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Human protein havi

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1 MAPWPELGDAQPNPDKYLEG......SREAQGRVPASDSKTECTAL 689
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	A human sodium pho	HOST-5 (NaPi-Iib)	Human ovarian canc	Human protein SEQ	Human Na-dependent	Human protein SEQ	Human sodium depen	Human polypeptide,	Human polypeptide,
SUMMARIES	ΙD	AAB18613	ABB50299	ABG96383	AAM78631	ABB12311	AAM79615	AAW77414	AAM93865	AAM93860
	89	21	22	23	22	22	22	13	22	22
	Query Match Length DB	689	689	689	069	700	700	069	631	397
οNο	Query	100.0	6.66	99.8	93.6	93.6	9.66	99.3	1.06	58.3
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Human sodium depen C glutamicum prote Corynebacterium gl Streptococcus poly Listeria monocytog Streptococcus pneu S. pneumoniae type Possible sodium-de Listeria monocytog Listeria monocytog Listeria monocytog Listeria monocytog Novel human diagno Novel human secret S. cerevisiae BAX- Pathogen specific Novel human diagno Human transporter Human transporter Drosophila melanog Novel human diagno Rovel human diagno	designated Npt2B. pt2B; intestinal epithelial cell; e metabolism; phosphatemia; sm; renal disease. 2B, useful e.g. for identifying
155 19 AAW77415 158 22 AAG92763 411 22 AAG92765 549 23 ABB29511 543 24 ABB29511 120 19 AAW77597 441 23 ABB47553 120 19 AAW77597 443 23 ABB4814 90 22 ABG27784 74 22 ABG23597 74 22 AAG27784 74 22 AAG27784 76 23 AAB11289 555 22 ABG11291 701 23 AAB24209 307 24 ABB81373 307 24 ABB81373 307 24 ABB66239 1743 24 ABB66239 1743 24 ABB66239 1743 24 ABG93114 456 24 AB119067 1120 22 ABG27785 509 23 ABG61543 896 22 ABG37786 728 ABG37786	entry)  entry)  hate cotransporter, dente cotransporter, My inorganic phosphate  s; hyperparathyroidis  -0014979.  11 S;  12 S;
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                                                                                                                          The present sequence represents a human sodium phosphate cotransporter, designated Npt2B. It is expressed on the apical surface of intestinal epithelial cells. Npt2B is a human type II protein, which is responsible for absorption and uptake of inorganic phosphate in the intestine. The protein is used to identify specific agonists and antagonists, and to raise antibodies. The agonists and antagonists are potentially useful for treating disease of inorganic phosphate metabolism, especially hyper- and hypo-phosphatemia, e.g. osteomalacia, rickets, hyperparathyroidism and renal disease.
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agents for treating hyper- and hypo-phosphatemia, and related nucleic
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                                                                         Fig 1; 42pp; English.
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                                                                            Claim 3;
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABAB3181-ABAB3182, ABAB3180, ABAB3181 and ABAB3183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour an epithelial ovarian tumour selected from service as every processing the energy of the methods can additionally be used to identify a particular tumour as serous expatadennocarcinoma, becased the energy of the methods can be account to the energy of the methods of the energy of the methods of the energy of the methods of the energy of t
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                                                                                                                                                                                                                    Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma undifferentiated carcinoma; clear cell adenocarcinoma; cystadenoma;
                                                                                                                                                                                                                                                                                                                                                                                                              adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE, immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ing and identifying ovarian tumor, identifying increased risk for ping ovarian cancer, and determining effectiveness of ovarian treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
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led by ovarian tumour marker genes of the invention.
                                                                                                                                                        HOST-5 (NaPi-lib) ovarian tumour marker protein, SEQ ID NO:147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 139-140; 140pp; English.
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                                                                                            (first entry)
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                                                             1 MAPWPELGBAQPNPDKYLEGAAGQQPTAPDKSKETNKNNTEAPVTKIELLPSYSTATLID
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186.66
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                 688; Conservative
Best Local Similarity
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Human, ovarian cancer, marker, cancer, familial history, brain disorder, central nervous system disorder, bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation, encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm, histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression from 363 cancer markers described in the narker is selected from 363 cancer markers described in the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer e.g. patients having a familial history of ovarian cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or parkinson's disease, brain cancer (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the historiac progression of ovarian cancer, monitoring the progression of ovarian cancer, certermining whether ovarian cancer has metastaized or is likely to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFFQGIGRLILLLGFLYFFVCSLDILSSA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient -
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                                                                                                                                                                                                                                                                                                                                3, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG,
Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB,
Iu K, Schmandt RE, Zhao X, Glatt K;
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Pred. No. 0;
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                                                                                                      14-MAR-2001; 2001US-276025P.
14-MAR-2001; 2001US-276026P.
10-ANG-2001; 2001US-311732P.
19-SEP-2001; 2001US-323580P.
26-SEP-2001; 2001US-325102P.
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                                                                                                                                                          The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW98329.AAM80302) that exhibit activity elating to erytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy, and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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Pred. No. 0;
1; Mismatches
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   Zhang J, Re
, Goodrich
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   Wang J,
Wejhrman
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Best Local Similarity 99.7
Matches 688; Conservative
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               Yang Y,
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2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0653561.
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20-JUN-2000; 2
19-JUL-2000; 2
01-SEP-2000; 2
15-SEP-2000; 2
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Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, athersoclarosis, coronary heart disease, cretical ischaemia, bone disorders (e.g., osteoporosis), and abnormal repair (or nucleic acids encoding then) may be used to promote wound repair (or nucleic acids encoding then) may be used to promote wound capair (or nucleic acids encoding then) may be used to promote wound content and fungal infections and ulcers), while those with a munomodulatory activities may be used in the treatment of viral, becreain and fungal infections in addition to immune disorders.

Companyabetides with growth factor addition to immune disorders.

Companyabetides with growth factor activity may be used in cell culture to give rise to neuropithelial cells capated and disease or accidental damage. The polypeptides may be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and mucleotides may also be used in the diagnosis of the above conditions, and in drug convening techniques. The present sequence represents a novel human conversed the suppartion.

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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemckinesis; thrombolysis; oncogenesis; proliferation; metastrasis; acancer; thmour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; chronic inflammatory condition; proliferative retinopathy; bone disorder; osteoporosis; vascular growth disorder; celeporosis; vascular growth disorder; cell culture; drug screening; gene therapy; antinflammatory; antiarthritic; haemostatic; antiarthritic; haemostatic; antiarteriosclerotic; antifungal; vulnerary; antiulcer.
Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Na-dependent phosphate transporter homologue, SEQ ID NO:2681
                                                                                                         660 APETFDNITISREAQGEVPASDSKTECTAL 689
                                                                                                                                                      661 APETFDNITISREAQGEVPASDSKTECTAL 690
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                                                                                                                                                                                                                                                                                                                                       ABB12311 standard; peptide; 700 AA
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27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-2002 (first entry)
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PRE12311
ABB12311
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ARB12311
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ARB12311
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119 LEITTQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDKKVISQIAMNDEKAKNKSLVK 299 311 IWCKTFINKTQINVTVPSTANCTSPSLCWTDGIQNWTWKNVTVKENIAKCQHIFVNFHLP 370 130 179 371 DLAVGTILLILSLLVLCGCLIMIVKILGSVLKGQVATVIKKTINTDFPFPFAMLTGYLAI 430 479 490 539 550 599 29 70 11 MAPWFELGDAQPNPDKYLSGAAGQQPTAPDKSKETNKTDNTEAPVTKIELLPSYSTATLI 60 DEPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFFQGIGRLILLLGFLYFFVCSLDILSS 71 DEPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFPQGIGRLILLIGELYFFVCSLDILSS 120 AFQLVGGKAAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSTSTVVSMVSSSLLTVRA 180 AIPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHY 300 IWCKTFINKTQINVTVPSTANCTSPSLCWTDGIQNWTWKNVTYKENIAKCQHIFVNFHLP 360 DLAVGTILLILSLIVILGGCLIMIVKILGSVLKGQVATVIKKTINTDFPFPFAWLTGYLAI 420 LVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTLGSNIGTTTTALLAALASPGNA 431 LVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTLGSNIGTTTALLAALASPGNA LRSSLQIALCHFFFNISGILLWYPIPFTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLI 540 PLIVEGISLAGWRVLVGVGVPVVFIIILVLCLRLLQSRCPRVLPKKLQNWNFLPLWMRSL 551 PLIVVEGLSLAGWRVLVGVGVPVVFIIILVLCLRLLQSRCPRVLPKKLQNWNFLPLWMRSL 491 LRSSLQIALCHFFENISGILLMYPIPFTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLI KPWDAVVSKFTGCFQMRCCCCCRVCCRACCLLCGCPKCCRCSKCCEDLEBAQEGQDVPVK 1 MAPWPELGDAQPNPDKYLBGAAGQQPTAPDKSKETNK-NNTBAPVTKIELLPSYSTATLI 99.6%; Score 3581.5; DB 22; Length 700; 99.7%; Pred. No. 0; 1. Mismatches 0; Indels 1; 660 APETEDNITISREAQGEVPASDSKTECTAL 689 Local Similarity 99.7 hes 688; Conservative 240 480 Query Match Matches 셤 qq a 8 g à 엄 ö g  $\delta$ g õ  $\dot{\delta}$ a ò g ⋩ ద ð ð 엄

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB0981-ABB12330 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host calls comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell and exactopolesis regulatory activity; tissue growth activity; hasematopolesis regulatory activity; tissue growth activity; chemotactic or chemokinentic activities; themosoulatory activities; the commondulatory activities; and provided in oncogenesis, cancer cell proliferation or metastasis.

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671 APETFDNITISREAQGEVPASDSKTECTAL 700

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell pooliteration or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; rissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 MAPWPELGDAQPNPDKYLEGAAGQQPTAPDKSKETNKTDNTEAPVTKIELLPSYSTATLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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Wang J, Zhang J, Ren F, Chen R, Wang :
Wejhrman T, Goodrich R;
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Pred. No. 0;
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              Ā
             AAM79615 standard; Protein; 700
                                                                                                       Human protein SEQ ID NO 3261
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01-SEP-2000; 200008-0654936.
15-SEP-2000; 200008-0663561.
20-OCT-2000; 200008-0693325.
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27-APR-2000; 2000US-0560875.
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Best Local Similarity
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Wang D,
Yang Y, W
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Zhao QA,
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DEPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFFQGIGRLILLIGFLYFFVCSLDILSS 119
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                                                                                                                                          191 AIPIIMGANIGTSITNTIVALMOVGDRSEFRRARARAGATVHDFFNWLSVLVLLDVEVATHY 250
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                71 DEPTEVDDPWNLPTLODSGIKWSERDTKGKILCFFQGIGRLILLLGFLYFFVCSLDILSS
                                                                                       131 APQLVGGKWAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSMVSSSILTVRA
                                                                                                                      180 AIPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHY
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                                                         120 AFOLVGGKMAGOFFSNSSIMSNPLLGLVIGVLVTVLVQSSS
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97US-0044974.
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The invention relates to primers for synthesising full length CDNA clones. 830 cDNRA molecules encoding a human protein have been clones. 830 cDNRA molecules esquences of 5'—and 3'—ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the Full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA assily without any special methods. The present sequence is a polypeptide encoded by a full length human CDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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601 KPWDAVVSKFTGCFQMRCCYCCRACCLI.CGCPKCCRCSKCCEDLIEBAQEGQDVPVK
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T, Koga ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; full length cDNA; cDNA synthesis; oligo-capping.
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K, Kojima S, Otsuki
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91.2%; Pred. No. 1.3e-301;
iive 1; Mismatches 0;
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Nagai F
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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su A, Sugiyama T,
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                                                                                                                                                                                                                                                    transporter IPT-1, as deduced from the nucleotide sequence of a cDNA clone (see AAV59498). It shows about 76% identity in 691 amino acids with bovine sodium dependent phosphate transporter and 55% identity in 625 amino adolum dependent phosphate transporter and 55% provided for the production of IPT-1 polypeptides in recombinant host cells. Such polypeptides can be used to raise antibodies and agonise the IPT-1 polypeptide. Agonists can be used to treat a subject in need of enhanced activity or expression of IPT-1, while antisgonists can be used to treat a subject having need to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity or expression of IPT-1. A claimed process for diagnosing a disease or susceptibility to disease related to IPT-1 expression or activity involves analysing for the presence or amount of IPT-1 expression in a sample. IPT-1 polypeptides and polynucleotides can be used for prevention, treatment and diagnosis of e.g. chronic renal failure, end-stage renal disease, uraemic bone disease and
                                                                                                                                                                                                                                     This is the amino acid sequence of human sodium dependent phosphate
                                                                                                      New DNA encoding sodium-dependent phosphate transporter protein IPT-1 - used to prevent, treat and diagnose e.g. chronic renal failure, end-stage renal disease, uraemic bone disease and cancer
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                                          1998-559435/48.
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                                                              N-PSDB; AAV77414.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been clones. 800 cDNA molecules encoding a human protein have been molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA asily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this parent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TAILAALASPGNALRSSLOIALCHFFINISGILLWYPIFFTRLPIRWAKGLGNISAKYRW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNWNFLPLWMRSLKPWDAVVSKFTGCFQMRCCCCCRVCCRACCLLCGCPKCCRCSKCCED 646
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                                                         synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 MNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGIQNWTMKNVTYKENI
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                                                                                                                                                                                                                                                                                                                                                                                                        58.3%; Score 2098; DB 22; Length 397; 98.3%; Pred. No. 2.8e-192; ive 0; Mismatches 1; Indels 6;
                                                                                                           Claim 8; SEQ ID NO 3955; 1380pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein having hydrophobic domain, HP03878.
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                                                       830 Primers useful for syntl
use in genetic manipulation
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        2001-524255/58
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 396; Conserv
                                                                                                                                                                                                                                                                                                                                                                       397 AA;
                       N-PSDB; AAK94816.
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AFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSMVSSSLLTVRA 179
                                                                               121 AFQLVGGKWAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSWVSSLLTVRA 180
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                                                                                                                                                     181 AIPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHY 240
                                                                                                                                                                                           LEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDKKVISQIAMNDEKAKNKSLVK 299
                                                                                                                                                                                                                300 IWCKTFINKTQINVTVPSTANCTSPSLCWIDGIQNWTMKAVTYKENIAKCQHIFVNFHLP 359
                                                                                                                                                                                                                                                                                      301 IWCKIPINKIQINVIVPSTANCISPSLCWIDGIQNWIMKNVIYKENIAKCQHIFYNFHLP 360
                                                                                                                                                                                                                                                                                                                                   DLAVGTILLILSLLVLCGCLIMIVKILGSVLKGQVATVIKKTINTDFPFPFAWLTGYLAI 419
                                                                                                                                                                                                                                                                                                                                                                                                    LVGAGMTFIVOSSSVFTSALTPLIGIGVITIERAYPLTLGSNIGTTTTAILAALASPGNA 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 KPWDAVVSKFIGCEQMRCCCCCKVCCRACCLLCGCPKCCRCCRCCEDLEEAQEGQDVPVK 601
                                                                                                                        180 AIPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHY
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T, Koga H;
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T, Nishikawa T, Isogai T, Hayashi K, Is
Wakamatsu A, Sugiyama T, Nagai K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660 APETFDNITISREAQGEVPASDSKTECTAL 689
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2000JP-0118774.
2000JP-0183765.
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                                                               496 SGILLWYPIPFTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIPLTVFGLSLAGWRVLV 555
                                                                                                                                                                                                                                                                                                       556 GVGVPVVFIIILVLCLRLLQSRCPRVLPKKLQNWNFLPLMWRSLKPWDAVVSKFTGCFQM 615
                                              316 PSTANCTSPSLCWTDGIQNWTWRNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVL
                                                                                                            CGCLIMIVKILGSVLKGQVATVIKKTINTDFPFPFAMLTGYLAILVGAGMTFIVQSSSVF
                                                                                                                             336 CGCLVLIVKLINSVLRGRVAQVVRTVINADFPFPLGWLGGYLAVLAGAGLIFALQSSSVF
                                                                                                                                                                            436 TSALTPLIGIGVITIERAYPLTLGSNIGTTTTAILAALASPGNALRSSLQIALCHFFFNI
                                                                                                                                                                                                                                                          SE AGILIMYLVPALRIPIPLARHFGVVTARYRWVAGVYLLIGFILLPLAAFGLSLAGGMVLA
                                                                                                                                                                                                                                                                                                                      New DNA encoding sodium-dependent phosphate transporter protein IPT-1 - used to prevent, treat and diagnose e.g. chronic renal failure, end-stage renal disease, uraemic bone disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPT-1; sodium dependent phosphate transporter; human;
kidney failure; kidney disease; uraemic bone disease; cancer;
diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human sodium dependent phosphate transporter IPT-1 variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW77415 standard; Protein; 155 AA
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                                                                                                                                                                                                                                                                                                                                                                     616 RCCCCCRVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 DSGIXWSERDTKGKILCFFQGIGRLILLIGFLYFFVCSLDILSSAFQLVGGKWAGQFFSN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemctactic and chemchinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LEGAAGQQPT--APDKSKETNKNNTEAPVTKIELLPSYSTATLIDEPTEVDDPWNLPTLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 95-96; 563pp; English.
                                                                                                                                                                                                                       PROT-) PROTEGENE INC.
(SAGA ) SAGAMI CHEM RES CENT.
                                                                                                                         06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000588.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0026862.
                                                                                          28-DEC-2000; 2000WO-JP09359
                                                                                                                                                                                         03-MAR-2000; 2000JP-0058367
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N-PSDB; AAD12586.
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Best Local Similarity
                                                                                                                                                                                                                                                                       Kato S, Kimura T;
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                              WO200149728-A2.
Homo sapiens.
                                                            12-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                            phosphate transporter into actual bypeptide, as deduced from the phosphate transporter into actual bypeptide, as deduced from the DNA sequence of a polymoclectide (see AAV59499) of the invention.

Methods are provided for the production of IPP-1 polypeptides (see also AAW77414) in recombinant host cells. Such polypeptides can be used to raise antibodies and also a claimed method for identifying compounds which inhibit or agonise the IPP-1 polypeptide. Agonists can be used to treat a subject in need of enhanced activity or expression of IPP-1, while antagonists can be used to treat a subject paving need to inhibit activity or expression of IPP-1. A claimed process for diagnosing a disease or susceptibility to disease related to IPP-1 expression or activity involves analysing for the presence or amount of IPP-1 expression in a sample. IPP-1 polypeptides and polymocleotides can be used for prevention, treatment and diagnosis of e.g. chronic renal failure, end-stage renal disease, uraemic bone disease and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GSNIGTTTTALLAALASPGNALRSSLQIALCHFFFNISGIILMYPIPFTRLPIRMAKGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 KKTINTDFPFPFAWLTGYLAILVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTL
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eda M, Ozaki A;
This is the partial amino acid sequence of a human sodium dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.6%; Score 742; DB 19; Length 155; 98.0%; Pred. No. 9.7e-63; o. Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum protein fragment SEQ ID NO: 6517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 NISAKYRWFAVFYLIIFFFLIPLTVFGL 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NISAKYRWFAVFYLIIFFFLIPLTVFAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG92763 standard; Protein; 388 AA.
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Ikeda M,
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2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organic acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AA;
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07-APR-2000;
03-AUG-2000;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 QLDKKVISQIAMNDEKAKNKSLVKIWCKTFINKTQINVTVPSTANCTSPSLCWTDGIQNW 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 TMKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGCLIMIVKILGSVLKGQVA 395
                                                                 sequences from the Corynetorm bacterium Corynebacterium glutamicum are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, mesuring expression amount and analysing the expression partiern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from Coryneform bacterium. Coryneform bacteria are useful for producing particularly incleic acids, vitamins, saccharides and organic acids, in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed Buropean Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 SIMDKVINPENSPKATILSNFWSFILGVLFTLMVTASSVTVASMOPVAASGGVVKOKPLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                        100 LILLLGFLYFFVCSLDILSSAFQLVGGKMAGQFFSNS--SIMSNPLLGLVIGVLVTVLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLVLLSILVIIIGINLILDGVYGF-----GTFSTTQMYQVAKDPLIGVLIGILATALVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 SSTSTSTVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMOVGDRSEFRRAFAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTLGSNIGTTTTAILAALASPGNALRSSLQIALCHFFFNISGILLWYFIP-FTRLPIRMA
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                     The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                    85;
                 Claim 17; SEQ ID NO: 6517; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                              11.6%; Score 418.5; DB 22; Length
26.9%; Pred. No. 4.3e-31;
tive 80; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum MCT protein SEQ ID NO:512
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AAB76765
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Streptococcus, GAS; GBS; group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                        211
                                                                                                           168
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                                                                                                                                                                                                                                                                                             330 DGIQNWTMKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGCLIMIVKILGSV 389
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                                                                                                                                                                                                                                                                                                                                                                  390 LKGOVATVIKKTINTDFPFPFAWLTGYLAILVGAGMTFIVQSSSVFTSALTPLIGIGVIT 449
                                                                                                                                                                                                                                                                                                                                                                                       215 TAATUTSIMDKVINPENSPKATILSNEWSFILGVLFTLMVTASSVTVASMQPVAASGVVK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                       450 IERAYPLTIGSNIGTTTTAILAALASPGNALRSSLQIALCHFFFNISGILLMYPIP-FTR 508
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                      152 VTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFRR
                                                                                          109 ATALVQSSTTTTLITVTVAVGTGIVSVPVAIPIILGANIGTTITAMLVAFSYVGERREFKR
                                                                                                                                               212 AFAGATVHDFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAP--DLLKVITKP
101 ILLIGFLYFFVCSLDILSSAFQLVGGKMA-----GQFFSNS--SIMSNPLLGLVIGVL
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                                                                                                                                                                                                                                                        229 Proligm--ngligsig-----hpsisaivc-----
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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395 VIIHLAEKTANLTAR 409
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(GENO-) INST GENOMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABN70142
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Tettelin H;
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AAF66082 and AAF68082 represent sequencing primers which are used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 876-877; 1119pp; English
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99DE-1040766.
99DE-1040830.
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99DE-1041378.
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99DE-1041395.
99DE-1042077.
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N-PSDB; AAF67998.
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 WO200100805-A2
                                                                      23-JUN-2000;
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09-JUL-1999;
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27-AUG-1999;
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                                                                                                                                                                                                                                       09-JUL-1999
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                                    04-JAN-2001
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Gaps

86;

Seguence Query Match

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treptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABN86644-ABN71256 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Wucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Mucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Attibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                             The invention relates to a protein (ABP25413-ABP30895) from group B
Claim 1; Page 3939; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins.
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## 549 AA; Sequence

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14;
                                                                 FFQGIGRLILLIGFLYFFVCSLDILSSAFQLVGGRMAGQFFSNSSIMSNPLLGLVIGVLV 152
                                                                                                                                     153 TVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFRRA 212
                                                                                                                                                                                                       213 FAGATVHDFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTK 272
                                                                                                                                                                                                                                          --- 123
                                                                                                                                                                                                                                                                        273 LIVQLDKKVISQIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGI 332
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                                                                                                                                                                                                                                                                                                                                                                   ---NFGRIIFGVGGIFFSINLM---GDAMDPLKSV-SAFON 173
                                                                                                                                                                                                                                                                                                                                                                                                              393 QVATVIKKTINTDFPFPFAWLTGYLAILVGAGMTFIVQSSSVFTSALTPLIGIGVITIER 452
                                                                                                                                                                                                                                                                                                                                                                                                                                          174 YLATL-----GDKPPQ-----GVFIGTALTMLIQSSAAIIGILQGLFSGGLLTLQG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 AYPLTIGSNIGTTTAILAALASPGNALRSSLQIALCHFFNISGILLWYPI--PFTRLP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 AIPILLGSNIGTCITAVLAAIGSNIAAKR----VAAAHVLFNLIGTIIFWILLVPFTSLM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 IRMAKGLG----NISAKYRWFAVFYLIIFFFLIPLTVFGLSLAGWRVLVGVGVPVVFII 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175;
   DB 23; Length 549;
                                                                                                                                                        SALIQSSSGVTVITVGLVSAGLLNIRQAIGIVMGANIGTTITSFLIG----
                                                                                                                                                                                                                                        ------FKLGDYALPMI
                                   Indels
7.8%; Score 280.5; DB 23; 22.4%; Pred. No. 1.3e-17; cive 70; Mismatches 140;
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332 LYL--DRLLITQAPSI 345
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              Local Similarity 22.4 es 111, Conservative
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Listeria monocytogenes protein #257.

(first entry)

05-FEB-2002

ABB47553;

ABB4753 ID ABB4 XX AC ABB4 XX XX DT 05-F DE List XX

ABB47553 standard; Protein; 544 AA.

RESULT 15

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The present invention relates to the genome sequence of listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primars for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein concoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 LIVQLDKKVISQIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGI 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 FQGIGRL-ILLIGFLYFFVCSLDILSSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFRRA
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                                                                                                                                                                                                                                                                                                                  C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; ernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; T, Domann E, Hain T, Berche P, Chribit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 274.5; DB 23; Length 544; 22.6%; Pred. No. 4.7e-17; ve 52; Mismatches 115; Indels 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IKLSEYSLPIIAVGAVLLFFFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; SEQ ID No 258; 192pp; French.
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Daniels J, Goece.
Daniels J, Goece.
Chakraborty T, Domann E, Ha
Ferez-Diaz J, Baquero F, G,
T Maduenio E, De Pablos B, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.6%;
Best Local Similarity 22.6%;
                                                                                                                                                                                           11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004629.
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Dussurget O, Chetouani F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 108; Conservative
                                                            Listeria monocytogenes.
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333 QNWTWKNVTYKENIAKCQHIFVNFHLEPDLAVGTILLILLILLILLALLVCGCLIMIVKILGSVLK- 391	FAW	160 LAGNESFHELTAQMSTNPFLGLLIGTIFTAVVQSSSATIGILQ 202	441 PLIGIGVITIERRAYPLITGSNIGTTTAILAALASPGNALRSSLQIALCHFFRNISGILL 500	203 ELYGÇGAIDLOAALPVLFGDNIGTTITAVLAAIGASVAAKRAAATHVIFNLIGAII 258	501 WYPIPFTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP 540	259 PMLILPLFTSIVAYLQGMFGINPEMTIAVAHGTFNITNTFIQFWFIGAFAMLVTKLIP 316	
333	392	160	441	203	501	259	
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Search completed: August 26, 2003, 15:50:04 Job time : 95 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 26, 2003, 15:48:07; Search time 49 Seconds (without alignments) 1352.249 Million cell updates/sec Run on:

US-10-052-664-1 3597 1 MAPWPELGDAQPNPDKYLEG......SREAQGEVPASDSKTECTAL 689 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283308 seqs, 96168682 residues Searched:

283308

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Match Ma		Description	sodium-dependent p	sodium/phosphate c	sodium/phosphate c	sodium/phosphate c	sodium/phosphate c	renal sodium-depen	hypothetical prote	nptA protein VC067	conserved hypothet	transport protein	Na/Pi cotransporte	conserved hypothet	hypothetical prote	conserved hypothet	conserved hypothet	Na+/Pi cotransport	hypothetical prote	transport protein	hypothetical 59.5	probable alpha hel	probable alpha hel	PTS system, Lichen	transporter BMBI07	conserved hypothet	probable membrane	PTS system, Lichen	Na+/Pi-cotransport	hypothetical prote
Query Score Match Length Di 2851 79.3 693 1706.5 79.3 693 1706.5 47.4 639 1682 46.8 653 1732.5 47.4 639 1882.5 46.8 642 732.5 20.7 15.6 382 283.5 7.6 554 2283.5 7.8 554 2283.5 7.8 554 2283.5 7.8 554 2283.5 7.8 554 2283.5 7.8 554 2283.5 6.7 559 218.5 6.1 5593 116.5 4.6 554 116.5 4.6 554 146.5 4.1 582 145.5 4.1 582 145.5 4.1 582 145.5 4.1 582 145.5 4.1 583 145.5 4.1 583	SOMMERIES	ID	\$49228	A48189	A54366	B48189	A54000	I46534	T27914	D82295	D89770	AB1178	E95057	G97926	G83825	E90554	H71283	F69952	A83819	AF1535	C65209	B91246	H86093	AB1542	AG3351	C82961	AI1011	AD1184	AD2852	B97629
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ਜਜ ਜ	40	Query Match	79.3	47.8	47.4	47.2	46.8	46.7	20.4	15.6	•	•	7.3	7.3	6.9	6.7	6.1	5.6	5.4	٠		•	4.5	4.1	4.1	4.1		4.0	3.9	9.0
Non Non Non Non Non Non Non Non Non Non		Score	2851	1721	1706.5	1698.5	1682	1681.5	732.5	559.5	283	274.5	263.5	262.5	247.5	242.5	218.5	203	o	179	165	191	161	146.5	146.5	146	145.5	142.5	139.5	139.5
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301 WCKTFINVTERNVTVPSPENCTSPSLCWTDGLYTWTIKNVTYKENIAKCQHIFVNFULSD 360

301 WCKTFTNKTQINVTVPSTANCTSPSLCWTDGIQNWTWKWVTYKENIAKCQHIFVNFHLPD

amino acid transpo	magnesium citrate	hypothetical prote	spovB related memb	hypothetical prote	hypothetical prote	periplasmic phosph	hypothetical prote	cytochrome-c oxida	cytochrome-c oxida	L-lactate permease	membrane protein [	conserved hypothet	NADH2 dehydrogenas	SNG1 protein - yea	hypothetical prote
H90447	A83743	AG1335	E97025	T24272	T18975	E64245	T15651	T11467	T13782	H84141	B95099	A97967	T14236	853920	B9006B
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520	442	443	539	164	152	654	188	511	513	524	307	307	498	547	456
3.8	3.8	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.5	3.5	3.5	3.5	3.5	3.5
136 3.8	135.5 3.8	133.5 3.7	132.5 3.7	131 3.6	ø	129 3.6	128 3.6		128 3.6	127.5 3.5	126.5 3.5			125 3.5	124.5 3.5

## ALIGNMENTS

-depende					
RESULT 1 S49228 sodium-dependent phosphate transporter - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999 C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999 C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999 C;Date: 10-Text_change 05-Nov-1999 R;Helps, C: Murer, H: McGivan, J. Bur. J. Biochem. 228, 927-930, 1995 A;Title: Cloning, sequence analysis and expression of the cDNA encoding a sodium-depende A;Reference number: 568972, MUD:9525303; PMID:7737195 A;Accession: 568972 A;Accession: S68972 A;Accession: Brelminary A;Molecule type: mRNA A;Residues: 1.693 <a href="https://december.ncbn">HEL&gt;</a> A;Cross-references: EMBL:X81699; NID:9547483; PIDN:CAA57345.1; PID:g547484	Ouery Match 79.3%; Score 2851; DB 2; Length 693; Best Local Similarity 76.3%; Pred. No. 1.1e-193; Matches 531; Conservative 82; Mismatches 73; Indels 10; Gaps 3;	QY 1 MARWPELGDAQENPDKXLEGAAGQQPTAPDKSKETINKUNNTEAPVTKIELLPSYSTATLID 60	QY 61 EPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFFQSIGRLILLLGFLYFFVCSLDILSSA 120	Qy 121 FQLVGGRAAGQPFSNSSIMSNPLAGLVIGVLVTVLVQSSSTSITSIVV8MVSSSLLTVRAA 180	QY 181 IPTIMGANIGTSITNTIVALMQVGDRSEFRRAPAGATVHDFFNNLSVLVLLPVBVATHYL 240

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sodium/phosphate cotransport protein, renal - North American opossum
C,Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American oposs
C,Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule V;pe: mRNA
A;Residues: 1-653 «SOR»
A;Cross-references: GB:L26308; NID:g425468; PIDN:AAA30978.1; PID:g425469
                                                                                                                                                                                                                                         J.; Biber,
                                                                                                                                                                                                         C;Accession: A54366
R;Sorribas, V.; Markovich, D.; Hayes, G.; Stange, G.; Forgo, J.; Bibe
J; B;Ol. Chem. 269, 6615-6621, 1994
J;Title: Cloning of a Na/P-i cotransporter from opossum kidney cells.
A;Reference number: A54366; MUID:94165050; PMID:7509808
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47.4%; Score 1706.5; DB 2;
Best Local Similarity 64.6%; Pred. No. 7.8e-113;
Matches 332; Conservative 72; Mismatches 93;
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Cispecies: Rattus norvegicus (Norway rat)
Cipate: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
Cipate: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
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Cipate: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change, U.; Stange, G.; Biber, J.; Murer,
Proc. Natl. Acession cloning of human and rat renal cortex Na/P-i cotransport.
A;Reference number: A48189; MUID:93317607; PMID:8327470
A;Accession: A48189
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                 LIVEGESLAGWRVLVGVGVPVVFIIIVVLCIRLLQSRCPRVLPKKLQNWNFLPLWMRSLK 600
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                                                                                                                                                                                          PWDKLITSLISCROMRCCCCCRVCCRLCCGLCGCSKCCRCTKCSEDLE---EGKDEPVKS 657
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59.9%; Pred. No. 7.1e-114;
iive 79; Mismatches 120;
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Best Local Similarity 59.9
Matches 348; Conservative
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Db 42 PGTSTASAISSLSPVTLTEHSCPCGEVLECHDPLPTKLAQEEBQXPEPRLSQKLAQVGT 99  Qy 96 GIGRLILLGFLYFFVGSLDILSSAFQLVGGKWAGQFFSNSSIMSNPLLGLVIGVLVTVL 155  :::	Qy 156 VQSSSTSTSIVVSMVSSSLLTVRAALPIIMGANIGTSITWTIVALMQVGDRSEFRRAFAG 215	QY 216 ATVHDFFWMLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIV 275	QY 276 OLDKKVISQIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDG 331  Db 280 QLDKSVITSIAVQDESLRNHSLIRIWCHPDTTEASTSMSRVEAIASLANTT 330	Qy 332 IQNWIMGNVIYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLGGCLIMIVKILGSVLK 391  Db 331	QY 392 GQVATVIKKTINTDEPEPFAMLTGYLALLVGAGMTFIVQSSSVFTSALTPLIGIGVITIE 451  Db 377 GQVANVIQKVINTDFPAPFTWVTGYFAMVVGASMTFVVQSSSVFTSAITPLIGLGVISIE 436	Qy 452 RAYPLTLGSNIGTTTTAILAALASPGNALRSSLQIALCHPFFNISGILLMYPIPFTRLPI 511  Db 437 RAYPLTLDSNIGTTTTAILAAVASPREKLSSSFQIALCHFFNISGILLMYPLPCTRLPI 496	QY 512 RMAKGLGNISAKYRWFAVFYLIIFFFLIPLITVFGLSLAGWRVLVGVGVPVVFIIILVLCL 571  Db 497 RMAKALGKRTAKYRWFAVLYILVCFLLLESLVFGISMAGWQANVGVGTPFGALLAFVVLV 556	QY 572 RILGSRCPRVLPKKLQNWNFLPLWARSLKPWDAVVSKFTGCF 613 :	9 9	renal sodium-dependent phosphate transporter type II - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999 C;Accession: 146534	R;Verri, T.; Markovich, D.; Perego, C.; Norbis, F.; Stange, G.; Sorribas, V.; Bib, Am. V. Physiol. 268, F826-F633, 1995 A, Pitle: Cloning of a rabbit renal Na-Pi cotransporter, which is regulated by die A;Reference number: 146534; MUID:95251013; PMID:7733319	4	F1D:ges//3/ 642;	CCDES 349; CODSETVATIVE 77; MISMATCHER 43 PVTKIELLPSYSTATLIDEPTEVDDFW 45 PGTSAYAPPSLSPVALFEHGCPYGRAREREP-	QY 87 KGKILCFPQGIGRLILLGFLYFPVCSLDILSSAFQLVGGKWAGQFFSNSSIMSNPLLGL 146	QY 147 VIGVLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDR 206	
A,Accession: B48189 A,Status: preliminary A,Misleoule type: mRNA A,Residues: 1-639 < MAG> A,Cross-references: GB:L13258; NID:g292349; PIDN:AAA36354.1; PID:g292350 C;Keywords: phosphoprotein; transmembrane protein	Query Match Best Local Similarity 58.7%; Ered. No. 2.8e-112; Matches 348; Conservative 82; Mismatches 118; Indels 45; Gaps 9;	OY 43 PVTKIELLESYSTATLIDEPTEVDDPWNLPTLQDSGIKWSERDTKGKILCF 93  DD 42 PGTSAYAFPSLGFVALAEHTCPCGEVLERHEPLPAKLALEEEQKPESRLVPK 93	QY 94 FQGIGRLILLLGFLYFFVCSLDILSSAFQLVGGKNAGQFFSNSSIMSNPLLGLVIG 149 :   ::   :	QY 150 VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEF 209  154 ILVTVLVQSSSTSTSIIVSMVSSGLEVSSAIPIIMGSNIGTSVTNTIVALMQAGDRTDF 213	OY 210 RRAFAGATVHDFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLIKVITKP 269  DD 214 RRAFAGATVHDCFNWLSVLVLLPLEAATGYLHHITRLVVASFNIHGGRDAPDLIKIITEP 273	Qy 270 FTKLIVQLDKKVISQIAMNDEKAKNKSLVKIWCKIFTNKTQINVTVFSTANCTSBSLCWT 329	OY 330 DGIONWIMKAVIYKENIAKCQHIFVNFHLEDLAVGTILLILSLLVLGGCLIMIVKILGSV 389  1	OY 390 LKGQVATVIKKTINTDEPEPEAMLIGYLALLVGAGNTFIVQSSSVFTSALTELIGIGVIT 449  DD 377 LKGQVAKVIQKVINTDEPAPETWVIGYEAMVVGASMIFVVQSSSVFTSAITPLIGLGVIS 436	Qy 450 IERAYPLTIGSNIGTTTTAILAALASPGNALRSSIQIALCHFFFNISGILLMYPIPFTRL 509  Db 437 IERAYPLTLGSNIGTTTTAILAALASPREKLSSAPQIALCHFFFNISGILLMYPVPCTRL 496	Qy 510 PIRWAKGLGNISAKYRWPAVFYLIIFFFLIPLTVFGLSLAGWRVLVGVGVPVVFIIILVL 569  497 PIRWAKALGKRTAKYRWFAVLYLLVCFLLLEPSLVFGISWAGWQVWVGVGTPFGALLAFVV 556	QY 570 CLRLLQSRCPRVLPRGCQNWNFLPLWMRSLKPWDAVVSKFTGCPQMRCCCCCR 622  :	RESULT 5 554000 sodium/chosphate cotransport protein remal cortex - mouse	C;Species: Mis musculus (house mouse) C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 17-Mar-1999 C;Accession: A54000	1994 oning, functional expression, tissue distribution, and in situ 54000; MUID:94350180; PMID:8070635	A;Scalus preliminary A;Molecule type: mmc A;Residues: 1-637 <col/> A;Cross-references: GB:L33878	Query Match 46.8%; Score 1682; DB 2; Length 637; Best Local Similarity 58.8%; Pred. No. 4.1e-111; Matches 342; Conservative 79; Mismatches 125; Indels 36; Gaps 5;	

us-10-052-664-1.rpr

DD 240  Qy 425 MTFIVQS.  ::   DD 275LIQS.  QY 485 QIALCHF  ::   DD 332 HWANCQY  QY 544 FGIGLAG  DD 392 IGFTLIP  DD 392 IGFTLIP  DD 392 IGFTLIP  DD 447 LQYYDPFI		1, R.R.; Mekalanos, U Nature 466, 477-483, A,Title: DNA Sequence A,Reference number: A A,Accession: D82295 A,Status: preliminary A,Molecule type: DNA A,Residues: 1382 <hb 1<="" a,cross_references:="" a,experimental="" a,gene:="" a,map="" c,genetics:="" g="" position:="" source="" th="" vc0676=""><th>Query Match Best Local Similari Matches 152; Cons Qy 58 LiDEPTE</th><th>Db 1 MINQATS 7; Qy 118 SSAFQLV</th><th> </th><th>Db 95 ETAIPMY OY 238 HYLEIIT</th><th>Db 155 GILEKVS OY 295 KSLVKIW</th><th></th><th>200 ag</th><th>Qy 415 GYL-AIL</th><th>Db 247 GPLHGIA</th></hb>	Query Match Best Local Similari Matches 152; Cons Qy 58 LiDEPTE	Db 1 MINQATS 7; Qy 118 SSAFQLV		Db 95 ETAIPMY OY 238 HYLEIIT	Db 155 GILEKVS OY 295 KSLVKIW		200 ag	Qy 415 GYL-AIL	Db 247 GPLHGIA
114	QY 507 TRLPIRMAKGLGNISAKYRWFAVPYLIIFFFLIPLTVFGLSLAGWRVLVGVGVPVVFIII 566	RESULT 7 T27914 hypothetical protein ZK563.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27914 R;Le, T. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid ZK563. A;Reference number: Z20439 A;Accession: T27914 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A;Residues: 1-504 <let> A;Cross-references: EMBL:U40061; PIDN:AAA81148.1; CESP:ZK563.2 C;Genetics: ZK563.2 A;Gene: CESP:ZK563.2 A;Gene: CESP:ZK563.2 A;Introns: 20/2; 47/1; 94/1; 138/1; 239/3; 275/3; 329/2; 371/3; 423/3</let>	Query Match 20.4%; Score 732.5; DB 2; Length 504; Best Local Similarity 30.0%; Pred. No. 3.9e-44; Matches 166; Conservative 110; Mismatches 148; Indels 129; Gaps 7	OY 65 VDDPWNLPTLQDSGIKWSERDTKGKILCFFQGIGRLILLLGFLYFFVCSLDILSSAFQLV 124  Db 29 VGDETBPPAHKKSIISWISTPTKHKVKYXITCSFLIFLILLVLFIYVCSLANMSTAFGLL 88	QY 125 GGKWAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSKVSSSLLTVRAAIPI1 184	QY 185 MGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDF7NWLSVLVLLFVBVATHYLEIIT 244	Qy 245 QLIVESPHFKNGEDAPDLLKVITKPFTKLIVQLDKKVISQIAMNDEKAKNKSLVKINCKT 304	305 FTNKTQINVTVBSTANCTSPSLCWTDGIQNWTWKNVTYKENIAKCQHIFVNFHLPDLAVG	Db 240 239	QY 365 TILLILSLLVLCGCLIMIVKILGSVLKGQVATVIKKTINTDFPFFFAMLTGYLAILVGAG 424

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HEI>
GB:AE004153; GB:AE003852; NID:G9655103; PIDN:AAF93841.1; GSPDB:GN00:
ce: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
seva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e of both chromosomes of the cholera pathogen Vibrio cholerae.
A82035; MUID:20406833; PMID:10952301
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                                                                                                                                                                                                   VGGKWAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSMVSSSLLTV 177
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------KLLDGHAANYVRNLLSKQCPGMWKPCTGYLVMLVG-- 274
                                       SSSVFTSALTPLIGIGVITIERAYPLTLGSNIGTTTTAILAALASPGNALRSSL 484
                                                                                                                       FFFNISGILLWYPIPFTR-LPIRMAKGLGNISAKYRWFAVFYLLIFFFLIPLTV 543
                                                                                                                                             TQLIVESFHPKNGEDAP---DLLKVITKPFTKLIVQLDKKVISQIAMNDEKAKN 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                    [imported] - Vibrio cholerae (strain N16961 serogroup O1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.6%; Score 559.5; DB 2; Length 382;
ity 30.7%; Pred. No. 4.9e-32;
iservative 83; Mismatches 141; Indels 119; Gaps
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                                                                                                                                                                                                                                                                                     VVSK-FT 610
                                                                                                                                                                                                                                                                                                                 : | ||
FMCKVFT 459
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C;Species: Streptococcus pneumoniae
C;Accession: B5557
R;Tettellin, H.; Melson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heic on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.S.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A55000; MUID:21357209; PMID:11463916
Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mc ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Fitle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Experimental source: strain TIGR4
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                                                                                                                                                                                                                                                                  A;Cross-references: GB:NC_003210; PIDN:CAC98904.1; PID:g16410215; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 LAGMESFHELTAQMST------NPFLGILIGTIFTAVVQSSSATIGILQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 PLIGIGVITIERAYPLTLGSNIGTTTTALLAALASPGNALRSSLQIALCHFFFNISGILL 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 FOGIGRL-ILLIGFLYFFVCSLDILSSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 TVLVQSSSTSTSTVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 LIVQLDKKVISQIAMNDEKAKNKSLVĶIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 QNWTMKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGCLIMIVKILGSVLK-
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A;Molecule type: DNA
A;Residues: 1-544 <GLA>
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A; Residues: 1-543 <KUR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                     Ogud
K.;
                                                                                                                                                                                                                                                           conserved hypothetical protein SA0100 [imported] - Staphylococcus aureus (strain N315)
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                                                                                                                                                                                                                                                                              C; Species: Staphylococcus aureus
C; Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D89770
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-555 «XUR»
A;Cross-references: GB:BA000018; PID:g13700020; PIDN:BAB41319.1; GSPDB:GN00149
A;Experimental source: strain N315
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           532
                                   307 AVSGEFAVFALQIALVHLSFNLMATVLIYGIPFLRELPIKGAELISTWACKSKMVVVSYL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 WLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDKKVIS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 QIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGIQNWTMKNVTYK 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89770
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         ASPGNALRSSLQIALCHFFFNISGILLWYPIPFTR-LPIRMAKGLGNISAKYRWFAVFYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 555;
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Pred. No. 2.5e-12;
7; Mismatches 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----WYPIPFTRLPIRMAKGLGNIS 521
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22.5%; Pred
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367 LGVFVVIPGSILALT 381
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A.Gene: SA0100
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Best Local S:
Matches 101
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OV 199 ATMOVGDRSEERRARAGATVHDFFNNISVITVI.PVEVATHVI.RTTTOT.TVRSEHFRNGED 248	155 ALING YOUNGERANGEROOM WIDE TANDS VEVELE VEVELUE BELLIKELI VEGET FRANCESE.	100 G	113 ALFWILTON TO THE TOTAL OF T	134FGVGGIFFALNLSMGR 379 LIMIVKILGSVLKGQVATVIKKTINTDFPFFRAMLTGYLALLVGAGNTFTVQSSSVFTSA : :     :     : :     : :	Db 156 MAPLKDLQVFKDYMIBLSKNPVLGVFVGTGLTLLIQASSATIGI 199 Qy 439 LTPLIGIGVITIERAYPLTLGSNIGTTTAILAALASPGNALRSSLQIALCHFFRNISGI 498	Db 200 iQNiyAGNLiDLQGALPVLFGDNIGTTTÄIIASIGANIAAKRVÄGAHVAFNIIGT 255  Qy 499 LLMYPIPFTRLPIRMAKGLGNISAKYRMPAVFYLIIFFFLIP 540 : : :	Db 256 VFCVIFLVPFTVLIHWFBATLALAPEMTIAFAHGTFNITNTIVQFPFIGALAYFVTKIIF 315	RESULT 13 G83825 hypothetical protein BH1407 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #text change 15-Jun-2001	C,Accession: G83825  R,Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir. Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and	A.Reference number: A83650, MUID:20512582, PMID:11058132 A.Accession: G83825, A.Status: preliminary A.Molecule type: DNA	A; KeBlondes: 1-543 < SIV> A; Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05126.1; GSPDB:GN00 A; Experimental source: strain C-125 C; Genetics: C; Genetics: BH1407			Qy 150 VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEF 209 ::	210 RRAPAGATVHDFFNWLSVLVLLPVBVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKP 1::::     107	QY         270 FTKLIVQLDKKVISQIAMNDEKARONKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWT 329           Db         130	OY 390 LKGOVATVIKKTINIDEPEFRANLTGYLALLUGAGMTFIVOSSSVFTSALTPLI 443
C; Genetics:	A,Gene: SP0496	Ouery Match 7.3%; Score 263.5; DB 2; Length 543; Best Local Similarity 22.5%; Pred. No. 5.9e-11; Matches 108; Conservative 53; Mismatches 134; Indels 185; Gaps 14;	OY 79 IKWSERDTKGKILCFFQGIGRLILLLGFLXFFVCSLDILSSAFQLVGGKNAGQFFSNSSI 138	QY 139 MSNPLIGIVIGVIVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIV 198	QY         199 ALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGED 258           Db         106 GFKLGNY 112		QY 319 ANCTSPELCWIDGIQNWTWRNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGC 378	379 LIMIVKILGSVLKGQVATVIKKTINTDFPFPFAMLTGYLA 156 MAPLKDLQVFKDTMIELSKNPVLG			iae (strain	off, B.S.	McAhren, S Jaskunas, S	A;Title: Genome of the Batterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G97926 A;Status: preliminary	A; Molecule type: DNA A; Residues: 1-543 < KUR> A; Cross-references: GB: AE007317; PIDN: AAK99243.1; PID: g15458006; GSPDB: GN00174 C; Genetics: A; Gene: spr0439	Ouery Match Best Local Similarity 22.7%; Score 262.5; DB 2; Length 543; Best Local Similarity 22.7%; Pred. No. 76-11; Matches 109; Conservative 52; Mismatches 134; Indels 185; Gaps 14;  Qy 79 IXWSENDTKGKILCFFQGIGRLILLGFLYFFVCSLDILSSAFQLYGGKMAGQFFSNSSI 138	139 MSNPLAGIVIGVLVIVQSSSTSTSIVVSMVSSLLFVRALPITMGANIGTSTTNTIV 146 TSNPPFGVLVGIGMTALIQSSSGVTVITVGLVSAGLITTRQAIGIVMGANIGTTVTSFLI

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C,Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
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                                                                                                                                                                                 Conserved hypothetical protein MYPU_3410 [imported] - Mycoplasma pulmonis (strain UAB CT C;Species: Mycoplasma pulmonis
C;Species: Wycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Aacession: E90554
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUD:21267165; PMID:11353084
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205 DQGAMDLFAALPVLFGDNIGTTITAVLAAIGASVAAKRA----ALTHVIFNLIGTIIVLI 260
                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL445566; PID:g14089755; PIDN:CAC13514.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 LVTVLVQSSSTSTSTVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 RAFAGATVHDFPNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPF 270
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conserved hypothetical integral membrane protein TP0771 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 LGYWEGI--LLVFVG-ISVFLMSIKMMSTSIRNVGSEKFKKIL--LSFSKRPIIGIFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 KGQVATVIKKTINTDFPFPRA-----WLTGYLAILVGAGMTFIVQSSSVFTSALTPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 --GIGVITIERAYPLILGSNIGTTTTAILAALASPGNALRSSLQIALCHFFFNISGILLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                             261 IIIPPTHPIAYLAEVFALNRPWTIAFAHGIFNVSNTIIQFPPIGILAIIV 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%; Score 242.5; DB 2; Length 569; 20.7%; Pred. No. 1.9e-09; ive 84; Mismatches 122; Indels 211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 20.79
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-569 <KUR>
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A;Genetic code: SGC3
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Riraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71283
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001248; GB:AE000520; NID:g3323074; PIDN:AAC65739.1; PID:g332307
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 KSKETNKNNT---EAPVTKIELLPSYSTATLIDEPTEVDDPWNLPTLQDSGIKWSERDTK 87
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Similarity 20.7%; Pred. No. 9.9e-08;
11; Conservative 78; Mismatches 149; Indels 199;
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Best Local Similarity 20.7*
Matches 111; Conservative
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August 26, 2003, 15:41:38; Search time 26 Seconds (without alignments) 1246.208 Million cell updates/sec
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1 MAPWPELGDAQPNPDKYLEG......srbaQGEVPASDSKTBCTAL 689
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt\_41:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Q06496 rattus norv	097704 ovis aries	homod					_						Q9wtw5 mus musculu	P46950 saccharomyc			Q36724 blattella g	Q9cmz9 pasteurella	Q8y773 listeria mo	P55017 homo sapien	P75185 mycoplasma						O79403 scyliorhinu	Q95918 polypterus	$\overline{}$		anopheles	P57381 buchnera ap
Set ING. HOS	ID		NPI2_RAT	NPT2 SHEEP	NPT2 HUMAN	NPT2 RABIT	NPT2 MOUSE	YOEW BACSU	YJBB_ECOLI	YJBB SALTY	YDI3_SCHPO	PSTA MYCGE	OCN3_HUMAN	COX1_LOCMI	LCTP BACHD	OCN3_MOUSE	SNG1_YEAST	OCN3 RAT	BOSS_DROME		NORM PASMU	MNTH LISMO	S123_HUMAN		COX1_RHISA		BOSS_DROVI	MNTH_LISIN	COX1_SQUAC	COX1_SCYCA	NUSM_POLOR	URAA_ECOLI		COX1_ANOGA	MFD_BUCAI
	DB	-	н	1	Н	<b>~</b> 1	М	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	<b>~</b>	Н	Н	rH	н	Н	Н	Ч	М	H	Н	Н	Н	H	Н	Н	H
	Query Match Length	1 1 1 1	637	639	639	642	637	310	543	543	630	654	556	512	524	551	547	551	896	508	464	448	1021	651	512	517	893	448	518	517	613	429	475	514	812
æ	Query Match	: :	47.8	47.7	47.2	46.7	46.3		4.6	4.0	9.8	3.6	•	•	3.5		3.5	3.4	3.4	•	3.3	3.5	3.5		3.5	3.2					3.1	3.1	3.1	3.	т. Г
	Score	1 1 1 1 1	1721	1717	1698.5	1681.5	1667	203	165	144.5	139.5	129	128.5	128	127.5	127	125	123.5	121.5	121	118	116	. 116	115	114	114	114	113	112.5	111.5	110.5	110	110	110	110
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P53114 saccharomyc 032086 bacillus su P33504 anopheles q Q27115 trypanosoma Q27115 trypanosoma P03921 mus musculu 09765 macaca mula Q44123 actinobacil P58295 rattus norv P26361 mus musculu 042196 xenopus lae
NUT1 YEAST YUBA BACSU COX1 ANOQU HT1 TRYYI NUTM MOUSE Y216 MYCPN SU54 MOUSE CKR8 MACMU ARUB ACTPL SGA5 RAT CFTR MOUSE CFTR MOUSE CFTR MOUSE CFTR MOUSE
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## ALIGNMENTS

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15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                       LEUCINE-ZIPPER.
PHOSPHORYLATION (BY PKC) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
34D02E7817683F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.8%; Score 1721; DB 1; Length 637; 59.9%; Pred. No. 1e-109; ive 79; Mismatches 120; Indels 34
                                    M3 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

M4 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

M5 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

M8 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
M2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Similarity
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NPT2 SHEEP STANDARD; PRT; 639 AA 097704; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update)

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Renal sodium-dependent phosphate transport protein 2 (Sodium/phosphate cotransporter 2) (Na(+)/Pi cotransporter 2) (Renal sodium-phosphate transport protein 2) (Renal Na(+)-dependent phosphate cotransporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 IMLSFLXLFVCSLDVLSSAPQLAGGKVAGDIFKDNAILSNPVAGLVVGILVTVLVQSSST
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                                                                                                                                                                                                                                                                                                                                                                                ovine renal outer cortex.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE INVOIVED IN ACTIVELY TRANSPORTING PHOSPHATE
INTO CELLS VIA NA+ COTRANSPORT IN THE RENAL BRUSH BORDER.
MEMBRANE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 ILLIGELYFFVCSLDILSSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEUCINE-ZIPPER.
PHOSPHORYLATION (BY PKC) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                         OVIS aries (Misego).
Bikaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea.
                                                                                                                                                                                                                                                                                                           IISSUE=Kidney cortex;
Wood I.S., Ford L.T., Penny J.I., Shirazi-Beechey S.P.;
"Characterisation of a Na+-dependent phosphate cotransporter from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M4 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
M5 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
M6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MI (POTENTIAL).
EXTRACELLUIAR (POTENTIAL)
M2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
M3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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or send an email to license@isb-sib.ch).
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Pfam; PF02690; Na Pi cotrans; 2.
TIGRFAMs; TIGR01013; 2a58; 1.
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Best Local Similarity 64.9
Matches 338; Conservative
                                                                                                                                                                                                    Bovidae, Caprinae, Ovis.
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Matches 348; Conservative
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93317607; PubMed-8327470;
Markovich D., Sorribas V., Stange G.,
Biber J., Marer H.,
Biber J., Marer H.;
"Expression cloning of human and rat renal cortex Na/Pi cotransport.";
Proc. Natl. Acad. Sci. U.S.A. 90:5975-5983 [1993].
-!- FUNCTION: MAY BE INVOIVED IN ACTIVELY TRANSPORTING PHOSPHATE
INTO CELLS VIA NA+ COTRANSPORT IN THE RENAL BROSH BORDER
                     FINALSVLVILDIERARIGYLHHITRLVVASFNIRGGRDAPDLLKIITBPFTKLIIQLDKSV
                                                              FNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDKKV
                                                  ISQIAMNDBKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGIQNWTMKNVT
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-1- TISSUE SPECIFICITY: KIDNEY, AND LUNG.
-1- SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                   LPKKLONWNFLPLWMRSLKPWDAVVSKFTGCFOMRCCCCCR
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01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Transport; Symport; Sodium transport; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUCINE-ZIPPER.
PHOSPHORYLATION (BY PKC) (POTENTIAL)
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:001521; F:sodium-dependent phosphate transporter acti.
GO; GO:0007589; P:fluid secretion; TAS.
GO; GO:0006798; P:phosphate metabolism; TAS.
GO; GO:0006717; P:phosphate metabolism; TAS.
InterPro; IPR003841; Na/Pi_cotransport; TAS.
Pfam; PF02690; Ma Pi_cotrans; 2.
TIGRPAMS; TIGR01013; Za58; 1.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                 M2 (POTENTIAL).

M3 (POTENTIAL).

M3 (POTENTIAL).

EXTRACELIGIAR (POTENTIAL).

M4 (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

M5 (POTENTIAL).

EXTRACELIGIAR (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

M6 (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

M7 (POTENTIAL).

EXTRACELIGIAR (POTENTIAL).

M8 (POTENTIAL).

M9 (POTENTIAL).

CYTOPLASNIC (POTENTIAL).

M8 (POTENTIAL).
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65D21D968C35D61B CRC64;
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M1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                Renal sodium-dependent phosphate transport protein 2 (Sodium/phosphate cotransporter 2) (Na(+)/Pi cotransporter 2) (Renal sodium-phosphate transport protein 2) (Renal Na(+)-dependent phosphate cotransporter 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biber J., Murer H., "Cloning of a rabbit renal Na-Pi cotransporter, which is regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T., Markovich D., Perego C., Norbis F., Stange G., Sorribas V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
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PHOSPHORYLATION (BY PKC) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                       570 CLRLLQSRCPRVLPKKLQNWNFLPLWMRSLKPWDAVVSKFTGCFQMRCCCCCR 622
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                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Am. J. Physici. 268:F626-F633(1995).
-!- FUNCTION: MAY BE INVOLUED IN ACTIVELY TRANSPORTING PHOSPHATE
INTO CELLS VIA NA+ COTRANSPORT IN THE RENAL BRUSH BORDER
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MS (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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Pfam; PP02690; Na Pi cotrans; 2.
TIGRFAMS; IIGR01013; 2a58; 1.
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MEDLINE=95251013; PubMed=7733319;
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16-0CT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Renal sodium-dependent phosphate transport protein 2 (Sodium/phosphate coransporter 2) (Na(+)/Pi cotransporter 2) (Renal sodium-phosphate transport protein 2) (Renal Na(+)-dependent phosphate cotransporter 2) (NaPi-7).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Q60825; Q62110; Q62111; Q62112; Q62113; Q62114; Q62115; Q62116;
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                                                                                                                                               51;
  333 N-LINKED (GLCNAC. . .) (POTENTIAL)
69431 MW; A48B8SC001642A8B CRC64;
                                                                                          DB 1; Length 642;
                                                                                        46.7%; Score 1681.5; DB 1; Length 58.6%; Pred. No. 4.9e-107; ive 77; Mismatches 119; Indels
N-LINKED (GLCNAC.
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642 AA;
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                                                        "Molecular cloning, functional expression, tissue distribution, and in
stel hybridization of the renal sodium phosphate (Na+/P(i))
transporter in the control and hypophosphatemic mouse.";
PASEB J. 8:862-869(1994)
                                                                                                                                                        MEDLINE=5629339; PubMed=8693007;
Martmann C.M., Hewson A.S., Kos C.H., Hilfiker H., Soumounou Y.,
Murer H., Tenenhouse H.S.;
"Structure of mutine and human renal type II Na+-phosphate
cotransporter genes (Npt2 and NPT2).";
Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414 (1996).
-!- FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE INTO
CELLS VIA NA+ COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Kidney.
-!- TISSUE SPECIFICITY: Kidney.
                                                                                                                        SEQUENCE OF 1-94; 110-177; 179-242; 254-312; 313-318; 332-333; 335-337
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LEUCINE-ZIPPER.
PHOSPHORYLATION (BY PKC) (POTENTIAL).
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Transport; Symport; Sodium transport; Transmembrane; Glycoprotein;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                      STRAIN=CS7BL/6J; TISSUB=Kidney cortex;
MEDLINE=94350180; PubMed=8070635;
Collins J.F., Ghishan F.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U56669; AAC52688.1; -...
EMBL: U56669; -; NOT ANNOTATED_CDS.
EMBL: U56670; AAC52689.1; -...
EMBL: U56671; AAC52690.1; -...
EMBL: U56672; AAC52691.1; -...
EMBL: U56673; AAC52692.1; -...
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Pfam; PF02690; Na Pi cotrans; 2.
TIGRFAMs; TIGR01013; 2a58; 1.
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EMBL, U56664; AAC52684.1; ALT_INIT.
EMBL, U56665; AAC52685.1; -.
EMBL, U56666; AAC52686.1; -.
EMBL; U56667; AAC52686.1; -.
EMBL; U26667; AAC52681.1; -.
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160 VQSSSTSTSIIVSWVSSGLLEVSSAIPIIMGSNIGTSVTNTIVALMQAGDRTDFRRARAG 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 IQNWTWKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGCLIMIVKILGSVLK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 RAYPUTLGSNIGTTTTALLAALASPGNALRSSLQIALCHFFFNISGILLWYPIPFTRLPI 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512 RMAKGLGNISAKYRWFAVFYLLIFFFLIPLTVFGLSLAGWRVLVGVGVPVVFIIILVLCL 571
                                                                                                                                                                                                                                                              43 PVTKIELLPSYSTATLID-----EPTEVDDFWNLPT-LQDSGIKWSERDTKGKILCPPQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Systematic sequencing of the 203 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many sporulation genes.";
Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                       42 PGTSTYAISSLSPVTLTEHSCPCGEVLECHDP--LPTKLAQEEEQKPEPRLSQKLAQVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168 / JH642;
MISDLINES-1724195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato I., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 RAYPLTLGSNIGTTTATLAAVASPREKISSSFQIALCHFFFNISGILLWYPLPCTRLPI
                                                                                                                                                                                                                                                                                                                                                                                 96 GIGRLILLLGFLYFFVCSLDILSSAFQLVGGXMAGQFFSNSSIMSNPLLGLVIGVLVTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 QLDKSVITSIAVGDESLRNHSLIRIWCHPDTTEASTSMSRVBAIGSLANTT-----
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                                                                                                                                                                                                             Gaps
                                 3
                                                                                                                                                                                                          36;
345 A -> D (IN REF. 2).

839 MSSRRSGTY -> NUIGKTINTD (IN REF. 444 G -> D (IN REF. 2).
68671 MW; 1796935971231C09 CRC64;
                                                                                                                                                                                                       80; Mismatches 126; Indels
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NCBI_TaxID=1423;
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                                                                                                                                              Score 1667; DB 1;
Pred. No. 4.7e-106;
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yqeW.
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                                                                                                                                                                                                       Matches 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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345
381
444
637 AA;
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A Kunst F., Gogaswara M. Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Brann M., Brighell S.C., Bron S.,
Bruchilet S., Bruschi C.V., Coldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Coldwell B., Capuano W.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chis Errington J., Fabret C., Errinis B., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Ruma S., Galizzi A., Galleron N.,
RA Hilbert H., Holsappel S., Hacono S., Hallo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hacono S., Hallo M.F., Itaya M., Mones L.,
RA Noris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Mone D., O'Reilly M., Ogawa K., Mixuno M., Moestl D., Nakai S., Noback M.,
RA Persecan E., Pulic P., Mixuno M., Moestl D., Nakai S., Noback M.,
RA Persecan E., Pulic P., Purnelle B., Rapoport G., Rey M., Serior S.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schleich S., Schreich S., Takamaru K.,
RA Taekcuchi M., Tamakoshi A., Taraka T., Taekamaru K.,
RA Taekcuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Visri A., Wabult R., Wandler E., Wedler H., Weitzenegger T.,
RA Tocato V., Uchiyama S., Vandenbol M., Vannier R., Vassarotti A.,
Vasia A., Waine A., Yanamoco H., Yanamaco K., Yata K.,
Perker P., Wipat A., Tamamoco H., Yanamaco K., Yata K.,
Poshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
R., Hell S., Weller E., Wanamoco C., Wellum Bacillus H., Helpe C., Wellum Bacillus H., Helpe C., Wellum P., Weller H., Weller E., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellum P., Wellu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: TO E.COLI YJBB.
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EMBL; D93717; BAA12081.1;

EMBL; Z99117; CAB14484.1;

PIR; F69952; F69952.

Subtilist; BG11647; Yagew.

InterPro; IPR004633; NaPi_cotranspt.

R Pfam; PF02690; Na Pi_cotranspt.

R TIGRPAMS; TIGR01013; Za58; 1.

R TIGRPAMS; TIGR01013; Za58; 1.

R TIGRPAMS; TIGR0104; NaPi_cotranspt.

M Hypothetical protein; Transmembrane; Complete proteome.

TRANSMEM 4 24 POTRNTIAL.
                       STRAIN=168 / JH642;
MEDILINE-97175542; PubMed=9023197;
HOWILL G., Masuda S., Mogk A., Kobayashi Y., Schumann W.;
"The dnak operon of Bacillus subtilis is heptacistronic.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26D45D3920C17D19 CRC64;
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                                                                                                                                                                                             MEDLINE=98044033; PubMed=9384377;
                                                                                                          Bacteriol. 179:1153-1164(1997)
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136
177
211
245
280
310 AA;
SEQUENCE FROM N.A.
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Gaps 14;
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                                                                                                                                                                                                                                                                                                                                                                               269 PFTKLIVQLDKKVISQIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCW 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ------FLTGRYPIKQLGTSFLGLGIFF--CISGFSHLAGP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 TIERAYPLILGSNIGTTTTAILAALASPGNALRSSLQIALCHFFFNISGILLWYPIPFTR 508
                                                                                             97 IGRLILLLGF---LYFFVCSLDIL----SSAFQLVGGKWAGQFFSNSSIMSNPLLGLVI 148
                                                                                                                                                                                            149 GVLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSE 208
                                                                                                                                                                                                                                                                                    209 FRRAFAGATVHDFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITK 268
                                                                                                                                                                                                                    329 TDGIQNWTMKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGCLIMIVKILGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 LTKLKTGADVLYHVND-----SNWSALLIGMVLTAIIHSSSVCIGILMSFMNEGIİ
                                                                                                                                           1 MNRMLILISFTALILSFLAGMNMLRKGLISMAYSKIBERLL--LFTD-----HPLKAFLI
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yana Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qlang B., Wen Y., Hou Y.,
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-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the Escherichia coli genome. IV. DNA sequence of the
5.6%; Score 203; DB 1; Length 310;
18.9%; Pred. No. 7.9e-07;
tive 74; Mismatches 126; Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.;
                                                                                                                                                                                                                                                                                                                                   ------LILGGLLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 AATGFVEQLSPDPAQKIAHFSLLFNVVTALLFLPLT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 LPIRMAKGLG-NISAKYRWFAVFYLIIFFFL-IPLT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=94089392; Pubmed=8265357;
                                                                                                                                                                                                                                                                                                                 108 -----DIVIWV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein yjbB. VJBB OR B4020 OR SF4086. Escherichia coli, and
                                                86; Conservative
Query Match
Best Local Similarity
Matches 86; Conserv
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YJBB_BCOLI
ID _YJBB_ECOLI
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein yibB.
                                                                                                                                                                                                                                                                                                                            MEDLINE=94110223; PubMed=8282693;
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96
119
154
195
216
294
59444 MW PO
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                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
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                                                         Salmonella typhimurium.
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                                                                                                                            SEQUENCE FROM N.A.
                                                                                               NCBI TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 STSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 DFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 -DLSWLSPLLI-----FIGVIFFLGR 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------IVQAVIPITQANGVQVI- 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FASLTGDILLDALIGAMFAIISYSSLAAVLLTATLTAAGIISFPVALCLV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 LGSNIGTTTTAILAALASPGNALRSSLQIALCHFFFNISGILLWYPIPFTRLPIRMAKGL 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 LILLIGFLYFFVCSLDILSSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 KTINTDFPFFFAMLTG--YLAILVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.6%; Pred. No. u.uuuss;
tive 58; Mismatches 134; Indels 170; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 543;
                                                                                                                                                EMBL; AB005417; AAA55910.1; -...
EMBL; AB015417; AAA5511.1; -..
EMBL; AB015417; AAA5511.1; -..
EVECOME, EG$209; C65209.
InterPro; IPR003841; Na/Pi_cotranspt.
InterPro; IPR004633; NaPi_cotranspt.
R TIGRPAMs; TIGR01013; ZaA8; 1...
R TIGRPAMs; TIGR01013; ZaA8; 1...
R TIGRPAMs; TIGR01014; ZaA8; 1...
Hypothetical protein; Transmembrans; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                              59466 MW; BA97149CC41A093F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 GKLSLPKAELVIYFHVFYNLVRCLVMLPFVDPMARF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 165; DB 1;
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-!- SIMILARITY: TO B.SUBTILIS YQEW
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P40730;
01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94; Conservative
                                                                                                                                          EMBL; U00006; AAC43114.1;
                                                                                                                                                                                                                                                                                                                                                                                                                543 AA;
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TRANSMEM
TRANSMEM
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PRANSMEM

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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 STSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQVGDRSEPRRAFAGATVH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 DFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDK 279
                                                                                                                                                                         STRAIN-LTZ / SGSC1412 / ATCC 700720;
MRDLINE-21534949; PubMed-11677609;
MCDLINE-21534949; PubMed-11677609;
MCDLINE-21534949; PubMed-11677609;
MCDLINE-21534949; PubMed-11677609;
MCDLITHON I., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Waterston R., Wilson R.L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LIHILISAVALLVWGTHIVRTGVMRVFGARLRTVLSR-SVEKKP-LAFCAGIGVTALVQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conlin C.A., Hakensson K., Liljas A., Miller C.G.;
Coloning and nucleotide sequence of the cyclic AMP receptor protein-
regulated Salmonella typhimurium pepE gene and crystallization of its
product, an alpha-aspartyl dipeptidase.";
D Bacteriol. 176:172(1994).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SUBCELLULAR: TO B.SUBTILIS YQEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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tive 53; Mismatches 134; Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 543;
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EMBL; U01246; -; NOT ANNOTATED_CDS.

Stydens, SG10492; yjba

InterPro; IPR00384; Na/P; cotranspt.

InterPro; IPR004633; NaPi_cotranspt.

Pfam; PF0269; Na Pi_cotrans; 1.

TIGRPAMS; TIGR001013; 2558; 1.

TIGRPAMS; TIGR00704; NaPi_cotranspt.

Hypothetical protein; Transmembrane; Complete proteome.
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434D9F724DFFEB67 CRC64;
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13;

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YJBB\_SALTY

103 -DLSWLSPLLI	
280 KVISQIAMNDEKAKNKSLVKINCKTFINKTQINVTVPSTANCISPSLCWTDGIQNWTWKN 339 123 K	CC entities requires a lic
, vering and vering an	EMBL; Z81312;
340 VTYKENIAKCCHIEVNFHLPDLAVGTILLILSLIVI.CGCLIMIVKILGSVIKGÇVATVIK 399 134	
	TRANSMEM 80
400 KIINIDEPEFERANDIG-YLALDGAGNIF VQSSSVFTSALDELGIGVIIEKAYPLT 457  164FASINGDIMLDALIGANFALISYSIAAVLITAATIIRPAGIISEPVALCIV 213	FT TRANSMEM 121 141 FT TRANSMEM 155 175 FT TRANSMEM 177 197
1.3SNTGTTTP11.aalaspgnalbss1.olai.Chppenisg11.1wyD1pptB1PTBM	TRANSMEM 209
	TRANSMEM 303 TRANSMEM 336
514 AKGLGNISAKYRWFAVFYLII 534	TRANSMEM 371 TRANSMEM 407
270 PKSELVIYFHVFYNLV 285	1 440 1 466 1 503
RESULT 9	TRANSMEM 575 SEQUENCE 630 AA;
YOUR STANDARD; PRT; 630 AA.	Query Match
01-N0V-1997 (Rel. 35, Created)	Best Local Similarity 20 Matches 140; Conservation
01-NOV-1997 (Rel. 35, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update)	Qy 6 ELGDAQPNPDKYLI
Hypothetical protein Clf8.03c in chromosome I. SPAC1F8.03C.	
Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	STOPTION OF DEWNITHINGS:
Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.	Db 56 DNSLQHRGY
NCBI_TaxID=4896;	Ov 111VC6
SEQUENCE FROM N.A. STRAIN=972;	Db 111 YATASPNRTSMIS
MEDLINE=21848401; PubMed=11859360;	
A. Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillindworth T., Chircher C.M.	Db 168 ASSTISAVVIGS
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalco, J., Hodgson G.	
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,	
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,	Ov 275 VOLD
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,	260
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,	Qy 302
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,	Db 318 LPFSLTSYAKNGW
BOLLYM A., Dangel I., Deck A., Delizati I., Relliatu K., Foli I.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,	Qy 317 STANCTSPSL-
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	Db 378 DFFYYLAGYLQSM
Ducas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Inode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,	ON 368 LILSLLVLCGCLI
Dominguez A., Revielta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	Db 430 RVFHRYKYLQIIG
Supakovski G.V., Ussery D., Barrell B.G., Nurse F.; "The genome sequence of Schizosaccharomyces pombe."; Matters als. G. (2007)	Qy 428 IVQSSSVFTSALT
Nacture 123:01.200(2002). -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential). -!- etwitabiru. beronce mo mus or soc/our.o.an/our.org.com.enality	Db 480 SVVGSQVSCQASV
This SWISS DDOWN of converient to is another three through a collaboration	Qy 478 NALRSELQIALCH
between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its	TO S33 EYLPSSINDTOVY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIKWSE--RDT-----KGKILCFFQGIGRL-----ILLLGFLYFF-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSLDILSSAFQLVGGKMAGOFFSNSSIMSNPL---LGLVIGVLVTVLV 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVFISI------GSSGLDYLNTLV----VGDLTSLKWRGF-- 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----C-KIFTNKTQINVIVP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKNPSMIAMMVVGGVILIAYSGYEMFIAPYPSCPRKVMNRTFITAVII 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----CWTDGIQNWTMKNVTYKEN---IAKCQHIFVNFHLPDLAVGTIL 367
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20.6%; Pred. No. 0.037;
ive 94; Mismatches 217; Indels 227;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=96026346, PubMed=7569993,

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fleischmann R.D., Bult C.J., Small K.V., Sandusky M., Fuhrmann J.L.,

Fleischmann D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Fleeterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing.",
J. Bacteriol. 175:7918-7930 (1993).

-!- FUNCTION: COLLD BE PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM FOR PHOSPHATE, PROBABLY RESPONSIBLE FOR THE TRANSLOCATION
OF THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM PERWEASE FAMILY. CYSTW SUBFAMILY.
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Eransport, Transmembrane; Complete proteome.
12
                                                                                                                                                                                                                                                                                                                                                Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                       Phosphate transport system permease protein pstA homolog.
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                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                             654 AA
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                                                                                                                                                                          PRT;
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MEDLINE=94075230; PubMed=8253680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000515; BPD transp.
Pfam; PF00528; BPD transp; 2.
PROSITE; PS00402; BPD TRANSP_INN
                               |:| |: |: |: |: 579 LVPAVSLSFIPLAAAFWQ 596
  538 LIP---LTVFGLSLAGWR 552
                                                                                                                                                                                                                         (Rel. 34, Created)
(Rel. 34, Last seq
(Rel. 41, Last ann
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                                                                                                                                                                             STANDARD;
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P47651;
01-OCT-1996
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Length 654;

DB 1;

Score 129;

3.6%;

Query Match

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26;
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                                                                                                                         71 LVSFIVSIGALIIASYIGVRTSFFLVYRCKPKIRKKLSLIIDILSGIPSVIFGLFASQIL 130
                                                                                                                                                                                                           ---SIFFRDILKLPPLSLIAVIAMLSFMIIPIVISLTTVINTLTYVINDL-ISVVVSLGENK 186
                                                                                                                                                                                                                                                                                245
                                                                                                                                                                                                                                                                                                                                TSAİYKIIKKEIKPQLTVILTLAFARAISETMAVNF------VLQSVNYQEVINN 235
                                                                                                                                                                                                                                                                                                                                                                                                                  236 NRFFTSDLKTLGSVISTFIFSENGDEQINGVLYIFGIIILILVSLLNFFAIWSANPKTLE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 VITKPFTKLIVQLDKKVISQIAMM-----DEKAKNKSLVKIWCKTFTNKTQINVTVPST 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 ANCTSPSLCWTDGIQN--WTMKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLIVLC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - NINBRSLFFKERLÖSTVWIKLNYFLK-----IFQELICTFLAFGFVLALLLFVFIN 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565
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                                                                                                                                                                              SNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIPIIMGANIGTSI 193
                                                                                                                                                                                                                                                                                                                                                                                     ------LIVESFHF-KNGEDA--------PDLLK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 GS--VAINNNGSTVFSFEADSTGRALVNTLVIILITITITFPLALLIALWLARYNNSKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEG FITSGLSSSN-----IFHLSLPGQTLTTRIYGQLFSINSNAISVMLETSLVSVVFLIL
                                                                            ILCFFQGIGRLILL-----LGFLYFFVCS------LDILSSAFQLVGGXMAGQFF
                                                                                                                                                                                                                                                                                194 INTIVALMQVGDRSE-----FRRAFAGATVHDFFNWLSVLVLLPVBVATHYLEIITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 IRTCQQALMNVSWDLRISAFALGISKREVIFKIVLPSALKGLIVALILSINRIIAETAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 RMAKGLGNISAKYRWFAVFYLIIFFFLIPLTVFG--LSLAGWRVLVGVGVPVVFIIILVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --RYPFLKKISNFIYQVVWFIPNNISALFVDLTSTRQSVKKI------KVN-----
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                             Gaps
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28-FEB-2003 (Rel. 41, Last annotation update)
Organic cation transporter 3 (Extraneuronal monoamine transporter)
(EMT) (Solute carrier family 22, member 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                          242; Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gruendemann D., Schechinger B., Rappold G.A., Schoemig E., "Molecular identification of the corticosterone-sensitive extraneuronal catecholamine transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTLGSNIGTTTTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE OF 513-556 FROM N.A., AND TISSUB SPECIFICITY.
MEDLINE=99134299; PubMed=9933568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570 CLRLLQSRCPRVLPKKLQNWNFLPLWMRSLKPW 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 AA.
                          97; Mismatches
  Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99212254; PubMed=10196521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCN3 HUMAN STANDARD; 1
075751; Q9UPO2;
28-FEB-2003 (Rel. 41, Last sequ
28-FEB-2003 (Rel. 41, Last sequ
28-FEB-2003 (Rel. 41, Last sequ
19.3%;
                          122; Conservative
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AND COPPER B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 VCSLDILSSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSTIVVSMV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 ILNIGELTGAFTL--GYAADRY---GRIVIYLLSCLGVGV------TGVVVAFA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 SSSLLTVRAAIPIIMGA-NIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFF----- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 PN--FPVFVIFRFLQGVFGKGTWMTCYVIVTEIVGSK---QRRIVGIVIQMFFTLGIIIL 257
Verhaagh S., Schweifer N., Barlow D.P., Zwart R., Carloning of the mouse and human solute carrier 22a3 (81c22a3/SIC222a3) identifies a conserved cluster of three organic cation transporters on mouse chromosome 17 and human 6q26-q27."
                                                                                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, SKELETAL MUSCLE,
PROSTAFE, AORTA, LIVER, FETAL LUNG, SALIVARY GLAND, ADRENAL GLAND,
KIDNEY AND BRAIN COFFEX. NO EXPRESSION DETECTED IN SPLEEN.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
                                                                                                                                                    TISSUE=Kidney; MEDLINE=20425388; PubMed=10966924; MEDLINE=20425388; PubMed=10966924; MLX., Huang W., Ganapathy M.E., Wang H., Kekuda R., Conway S.J., Libbach F.H., Ganapathy V.; Rithoution of the organic cation transporter OCT3 in the kidney."; Am. J. Physiol. 279:F449-F858(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                      FUNCTION: Mediates potential-dependent transport of a variety of organic cations. May play a significant role in the disposition cationic neurotoxins and neurotransmitters in the brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 128.5; DB 1; Length 556; 
; Pred. No. 0.18; 
63; Mismatches 173; Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 604842; -. Gintegral to plasma membrane; TAS. GO; GO:0005687; C:integral to plasma membrane; TAS. GO; GO:0005624; C:membrane fraction; TAS. GO; GO:001519; F:organic cation transporter activity; TAS. GO; GO:0015695; P:organic cation transport; TAS. InterPro; IPR007114; MFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004149; Orgat transp.
InterPro; IPR005828; Sub transporter.
InterPro; IPR005828; Sub transporter.
InterPro; IPR00883; Sugar tr; 1.
ICRPAMS; TICR00898; 2A0119; 1.
PROSITE; PS00216; SUGAR, TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR, TRANSPORT 2; FALSE NEG.
Transport; Ion transport; Transmembrane; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                 FUNCTION, AND TISSUE SPECIFICITY.
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                                                                                        Genomics 55:209-218(1999).
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-----NW--LSVLVLLPVEVATHYLEIITQ----LIVESFHFKNGEDAPDLLKVITK 268
                                                    258 PGIAYFIPNWQGIQLAITLDSFLFILIYWVVPBSPRWLITR----KKGDKALQILRRIAK 313
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J. Mol. Evol. 41:1928-941(1955).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAN CANALYZES THE REDUCTION OF OXYGEN TO WATER. SUBGNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBGNIT OF THE ENZYME ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBGNIT 2 AND HEMB A OF SUBGNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 FTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIPLTVFGL--SLAGWRVLV----GVG
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-:- SUBCELIULAR LOCATION: INVEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE. COMPAINS 12 POTEMTIAL TRANSMEMBRANE DOMAINS.
-:- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                               314 CNGKYL----SSNYSEITVTDEEVSNPSFLDL-------VRTPQMRKCTLILMF-
                                                                                                                                                                                                                                                                                                                                  329 TDGIQNWTMKNVTYKENIAKCQHIFVNPHLPDLAVGTILLILSLLVLCGCLIMIVKILGS
                                                                                                                                                                                                                                                                                                                                                                             ----AMFTSAVVYQGLVMRLGIIGGNLYIDFPISGVVELPGALLIL----LTIERLGR
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                                                                                                                                                                 269 PFTKLIVQLDKKVISQIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCW
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MEDLINE-96139026; PubMed=8587138;
Flook P.K., Rowell C.H.F., Gellissen G.;
"The sequence, organization, and evolution of the Locusta migratoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha,
Acridoidea, Acrididae, Oedipodinae, Locusta.
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15-SEP-2003 (Rel. 42, Last annotation update)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1).
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(Rel. 38, Last seq
(Rel. 42, Last ann
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Fuji F., Hira
Horikoshi K.;
             28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport;
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Best Local S:
Matches 83
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TRANSMEM
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                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                  1'-histidyl-3'-tyrosine (By similarity)
                                                                                                                                                                                             IRON (HEME A3 AXIAL LIGAND) (PROBABLE) .
IRON (HEME A AXIAL LIGAND) (PROBABLE).
                                                                                                                               (PROBABLE)
                                                                                                                                                                                                                                                           3.6%; Score 128; DB 1; Length 512;
20.1%; Pred. No. 0.18;
.ive 61; Mismatches 150; Indels 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 KGQVATVIKKTINTDFPFP-----FAWLTG----YLAILVGAG----
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PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
                                                                                                                               LIGAND)
                                                                                                                                                                                                                                  98031A229B00511C CRC64;
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
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                                                                                                                  Respiratory chain; Inner membrane.
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                                                 InterPro; IPR000883; COX1. Pfam; PF00115; COX1; 1.
             EMBL; X80245; CAA56527.1;
PIR; T11467; T11467.
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473 ESMIKOR 479
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STRAIN-C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the alkaliphilic bacterium Bacillus
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                                                                                                                                          L-lactate permease.
LCTP OR BH3936.
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                                                                             ---SPFYLLTMFVFLWSLP--AFKGLLAEGGALE 326
                                                --AVGTILLILSLLVLCGCLIMIVKILGSVLKGQVATV 397
                                                                                                                                    398 IXKTINTDFPFPFAM---LIGYLALLVGAGMTF----IVQSSSVFTSALTPLIG-IGVI- 448
                                                                                                                                                              FUNCTION: Mediates potential dependent transport of a variety of organic cations. May play a significant role in the disposition of cationic neurotoxins and neurotransmitters in the brain.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN KIDNEY CORTEX BUT NOT MEDULAL. LOW LEVELS. FOUND IN BRAIN. IN THE KIDNEY, EXPRESSED SPECIFICALIX IN THE PROXIMAL AND DISTAL CONVOLUTED TUBULES AND WITHIN BOWMAN'S CAPSULE BUT NOT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: LEVELS ARE HIGH DURING GESTATION BUT DECREASE GREATLY TOWARDS THE END OF GESTATION. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Kidney;
MU X., Huang W., Ganapathy M.E., Wang H., Kekuda R., Conway S.J.,
Leibach P.H., Ganapathy W.;
Structure, function, and regional distribution of the organic cation
transporter OCT3 in the kidney. ".
Am. J. Physiol. 279:F449-F458(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Verhaagh S., Schweifer N., Barlow D.P., Zwart R.;
"Cloning of the mouse and human solute carrier 22a3 (Slc22a3/SlC22A3)
identifies a conserved cluster of three organic cation transporters
on mouse chromosome 17 and human 6q26-q27.";
Genomics 55:209-218(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                               св-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Organic cation transporter 3 (Solute carrier family 22, member 3).
SLC22A3 OR OCT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus
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STRAIN=CD-1; TISSUE=Placenta;
MEDLINE=99134299; PubMed=9933568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
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                                                                                                                                                                                                                                                          435 TGSVVNNNTLFAPIQTTAGAIIGTNPSLLVAANTAGG 471
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                             -COHIFVNFHLPDL--
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290 LKDVIKAW-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 OMFFT-LGIIILDGIAYFTPSWQGIQLAISLPSFLFLLYYWVVPESPRWLITRKQGEKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 TS-TSIVVSMVSS-SLLIVRAAIPIIMGANIGTSITNTIVALMQVGDRŞEFRRAFAGATV
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InterPro; IRR005828; Sub transporter.
InterPro; IRR005829; Sug transporter.
InterPro; IRR003639; Sugar transpt.
InterPro; IRR00363; Sugar transpt.
IRRAPMs; ITGR00898; Za0119; I.
PROSITE; PS000216; SUGAR TRANSPORT 1; 1.
PROSITE; PS000217; SUGAR TRANSPORT 2; FALSE NEG.
Iransport; Ion transport; Transmembrane; Glycoprotein.
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ID SNGI_YEAST STANDARD;
AC P46950;
DT 01-NOV-1995 (Rel. 32, Created)
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hes 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces cerevisiae chromosome VII contains four previously unknown open reading frames.";
Yeast 11:1087-1091 (1995).
-!- FUNCTION: MAY FUNCTION AS A N-METHYL-N'NITRO-N-NITROSOGUANIDINE (MNNG) EXPORT PERMEASE.
                    01-NOV-1997 (Rel. 35, Last annotation update)
Nitrosoguanidine resistance protein SNG1.
SNG1 OR YGR197C OR G7591.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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20.1%; Pred. No. 0.31;
tive 85; Mismatches 229; Indels 188;
                                                                                                                                                                                                                       MEDIJINE-95272615; PubMed=7753113;
Grey M., Pich C.T., Haase E., Brendel M.;
"SNG1 -- a new gene involved in nitrosoguanidine resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                             Guerreiro P., Maia e Silva A., Barreiros T., Arroyo J.,
Garcia-Gonzalez M., Garcia-Saez M.I., Rodrigues-Pousada C.,
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A -> V (IN REF. 1).
D4421BA2DED55420 CRC64;
Last sequence update)
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Mutat. Res. 346:207-214(1995)
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EMBL; X82775; CAA58016.1; -.
EMBL; Z72982; CAA97224.1; -.
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SGD; S0003429; SNG1.
GO; GO:0042493; P:response
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224 SLISQDANSEFNSSIFFESVFESGRDPSSVKSTILPLMQQLEVRLQXYYVKEY-----
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        193 ITNTIVALMQVGDRSEFRRAFAGAT-
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August 26, 2003, 15:47:17; Search time 118 Seconds (without alignments) 1506.765 Million cell updates/sec
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1 MAPWPELGDAQPNPDKXLEG......SRBAQGEVPASDSKTECTAL 689
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			Description	O900v7 homo sapien	095436 homo sapien	Q8wya9 homo sapien	Q9jj09 rattus norv	Ogdbp0 mus musculu	092290 mus musculu	Q27960 bos taurus	Q8n2k2 homo sapien	O9pt82 xenopus lae	O9pt83 xenopus lae	Q9ddr7 cyprinus ca	091237 pseudopleur	Q9dds6 brachydanio	O9ptq8 brachydanio	Q9d2v6 mus musculu	Q28361 didelphis m
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61 BPTEVDDPWNLPTLQDSGIKWSERDTRGKTLCFFQGIGRLILLLGFLYFFVCSLDILSSA 120

1 MAPWPELGDAQPNPDKYLRGAAGQQPTAPDKSKETNKNNTBAPVTKIELLPSYSTATLID 60

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2.00.00.10.00.00.00.00.00.00.00.00.00.00.		PRELIMINARY	-2000 (TrEMBLrel. 15 -2000 (TrEMBLrel. 23 -2003 (TrEMBLrel. 23 dependent phosphate	oa; 1a;	intestine; lift; pubMed=10610 'Collins J.F., G coning, functional al localization o i+-Pi) transporter 181-284(1999).	1001450; 4F 1003841; Na 1003841; Na 1003; Na 1001013; Na 1198; 4FE45 1198; 4FE45	Similarity 99. 18; Conservative
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RA XM. H., Bad. L., Collins J.F., Ghishan F.K.;

RT "Molecular cloning, functional characterization of a human intestinal RT "Molecular cloning, functional characterization of a human intestinal RT sodium-phosphate transporter gene promoter and its gene structure.";

RI sodium-phosphate transporter gene promoter and its gene structure.";

RI sodium-phosphate transporter gene promoter and its gene structure.";

RI EMBL; AF234245; AAL55657.1;

DR EMBL; AF234238; AAL55657.1; JOINED.
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                                             MAPWPELGDAQPNPDKYLEGAAGQQPTAPDKSKETNK-NNTEAPVTKIELLPSYSTATLI
                                                                      1 MAPWPELGDAQPNPDKYLEGAAGQQPTAPDKSKETNKTDNTEAPVTKIELLPSYSTATLI
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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EPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFFQGIGRLILLLGGFLYFFVCSLDILSSA 120
                                         PQLVGGKWAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSTVVSMVSSSLLTVRAA 180
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A Felld J.A., DellaPenna K.A., Edwards R.M.;

Felld J.A., DellaPenna K.A., Edwards R.M.;

Toloning and characterization of a sodium dependent phosphate

T transporter isoform expressed in human small intestine and lung.";

T transporter isoform expressed in human small intestine and lung.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL, ARVIL1856; ARC9855.1;

R Genew, HGNC:11020; SLC34A2.

R InterPro; IPR001450; 4F845 ferredoxin.

InterPro; IPR001450; 4F845 ferredoxin.

R FIGRPAMS; TIGR01013; 2a58; 1.

R TIGRPAMS; TIGR01013; 2a58; 1.

R PROSITE; PS00198; 4F846; FERREDOXIN; 1.

SEQUENCE 690 AA; 75761 MW; BAC4F7D1C992D5C0 CRC64;
                                                                    FQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSIVVSMVSSSLLTVRAA
                                                                                                                    IPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHYL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3570.5; DB 4; Length 690; Pred. No. 7.9e-251;
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1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-1993 (TrEMBLrel. 23, Last annotation update)
Sodium dependent phosphate transporter isoform NAPI-3B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
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01-MAY-1999 (
01-MAY-1999 (
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                        Cotransporter
                                                                                                                                                                              81.3%; Score 2926; DB 11; Length
80.5%; Pred. No. 4.9e-204;
Live 66; Mismatches 64; Indels
                                                   Am. J. Pathol. 157:21.27(2000).

EMBL; AF157026; AAF76291.1; -.

InterPro; IPR003841; Na/Pi_cotranspt.

PIGRAM, FP02609; Na_Pi_cotrans; 2.

FIGREMS; TIGRO1013; 2a58; 1.

SEQUENCE 695 AA; 75992 MW; 3FAFB827527E0061 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Solute carrier family 34 (Sodium phosphate), member SEC34A2.
Mus musculus (Mouse).
                      Type IIb Na/Pi
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     Tanaka M., Sugimura H.;
"Isolation and Localization of
Developing Rat Lung.";
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                                                                                                                                                                            Query Match
Best Local Similarity 80.5
Matches 545; Conservative
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAINFWISTERT, TISSUE-Lung;
MEDLINE-20340494; PubMed=10880371;
Hashimoto M., Wang D.-Y., Kamo T., Zhu Y., Tsujiuchi T., Konishi
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                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                  Length
                                                                                                                                                               64789 MW; 32AECE5C2B5098A7 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
Type IID sodium-phosphate transporter.
Rattus norvegicus (Rat).
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                                                                                                                                                                                                  Score 3023; DB 4;
Pred. No. 3.6e-211;
                                                                                                                                                                                                                                 1; Mismatches
EMBL; AF234239; AAL55657.1; JOINED.
EMBL; AF234241; AAL55657.1; JOINED.
EMBL; AF234243; AAL55657.1; JOINED.
EMBL; AF2342443; AAL55657.1; JOINED.
INTERPOSSION NA PL COLTAINSD.
Pfam; PF02690; NA PL COLTAINSD.
TIGREPAS; TIGREPAS; TARGAUGI3; Za58; 1.
NON TER

SEQÜENCE 591 AA; 64789 NW; 32AECESC
                                                                                                                                                                                                84.0%;
                                                                                                                                                                                                Query Match
Best Local Similarity 99.8
Matches 590; Conservative
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VKASGAFDNAAMSKECQDE
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Matches 541; Conservative
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                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             SLC34A2 OR NPT2B
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                                                                                    Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Fukuda S., Alizawa M., Nishi K., Kiyosawa H., Kondo S., Famanaka I., Saito T., Odazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Relistenhann W., Gassterland T., Gissi C., King B., Kochiwa H., Steinhi L.M., Staubli F., Suzuki R., Tomita M., Nagner L., Nashio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brostein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Korone P., Ring B., Ringwald M., Rozarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Chordata; Craniata; Vertebrata; Buteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                      'Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.8%; Score 2905; DB 11; Length 697;
80.0%; Pred. No. 1.6e-202;
ive 62; Mismatches 70; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003841; Na/Pi_cotranspt.
Pr02690; Na Pi_cotrans; 2.
TIGREAMS; TIGR01013; 2a58; 1.
SEQUENCE 697 Ap; 76244 NW; 2a7B9384857BF16F CRC64;
                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
EMBL; AK004832; BAB23600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0%
Watches 543; Conservative
                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1342284; Slc34a2.
Metazoa;
Eutheria;
                         NCBI_TaxID=10090;
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60 DEPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFFQGIGRLILLLGFLYFFVCSLDILSS
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                                                                                    KPWDAVVSKFTGCFQMRCCCCCRVCCRACCLLCGCPKCCRCSKCCBDL--EEAQEGQDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of a murine type II sodium-phosphate cotransporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=NWRI, TISSUE-Small intestine;
MEDLINE=99045724; PubMed=9826740;
Hilfiker H., Hattenhauer O., Traebert M., Forster I., Murer
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MGD) MGI:13422841; Na/Pi cotranspt.
Dfam; PF02690; Na_Pi_cotrans; 2.
TIGREAMS; TIGRO1013; 2a58; 1.
STRITENCE 697 AA; 76286 MW; 839E5CCB0F565265 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Type IIb Na/phosphate-cottansporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in mammalian small infestine.";
Proc. Natl. Acad. Sci. U.S.A. 95:14564-14569(1998)
EMBL; AF081499; AAC80007.1; -.
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    241 ERLTNLVVESFHFROGEEAPELLKVITDPFTKLIIQLDKSILNQIAMNDESVQNKSMIKI 300
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                                                                               301 WCKTFTNVTERNVTVPSPENCTSPSLCWTDGLYTWTIKNVTYKENIAKCOHIFVNFNLSD
                                                                                                                                                              361 AIVGTILLITSLLILCTCLILIVKLLGSVLRGQVAAVIKKTINTDFPYPFSWVTGYLAIL
                                                                                                                                                                                                                                 VGAGMIFIVOSSSVFISALIPLIGIGVITIERAYPLILGSNIGITITAILAALASPGNAL
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                                                                                                                                      361 LAVGTILLILSLLVLCGCLIMIVKILGSVLKGOVATVIKKTINTDFFFFFAWLTGYLAIL
                                                                                                                                                                                                                                                                                                                     481 RSSLQIALCHFFFNISGILLMYPIPFTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9
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397 Aa; 43726 MW; 23D42CBFC9555458 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ90534.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 PETFDNITISREAQ----GEVPASDSK--TECTAL 689
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                                                                                                                                  480 LRSSLQIALCHFFFNISGILLMYPIPFTRLPIRMAKGLGNISAKYRWFAVFYLIIFFFLI
                                                                                                                                                                                                                             PLIVFGLSLAGWRVLVGVGVPVVFIIILVLCLRLLQSRCPRVLPKKLQNWNFLPLWMRSL
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID=9913;
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Helps C.R., Murer H., McGiven J.D.;
Cloning, sequence analysis and expression of the cDNA encoding is sodium-dependent phosphate transporter from the bovine renal epithelial cell line NBL-1.";
EML: J. Blochem. 229.27-930(1995).
EML: X81699; CAA27345-1.;
InterPro; IRR003841; Na/Pi cotranspt.
Pfam; PR02690; Na_Pi cotrans; 2.
TIGRRAMs; TIGRO1381; Na/Pi cotrans; 2.
TIGRRAMS; TIGRO1381; Na/Pi cotrans; 3.
SEQUENCE 693 AA; 75826 WW; GELCCI7FE5C13213 CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-MR-2003 (TrEMBLrel. 23, Last annotat
Sodium-dependent phosphate transporter.
Bos taurus (Bovine).
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                                                      342 CSHLFASTNLFDLAVGLILLALSLFVLCVCLILLVKILNSLLKGQVSVLIKKVINTDFPF
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                                                                                                                                                  KNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGIQNWTMKNVTYKENI----AK
                                                                                                                                                                                                                                                                         349 COHIFVNFHLPDLAVGTILLILSLLVLCGCLIMIVKILGSVLKGQVATVIKKTINTDFPF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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XNAPI-A.
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NCBI_TaxID=8355;
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MEDLINE=97248089; PubMed=9094212;
Ishizuya-(Na. A., Stolow M.A., Ueda S., Shi Y.B.,)
"Temporal and spatial expression of an intestinal Na+/Po4 3-
cotransporter correlates with epithelial transformation during thyroid
hormone-dependent frog metamorphosis.";
Dev. Genet. 20:53-66(1997).
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                               121 PFPPAWLIGYLAILVGAGMTFIVQSSSVFTSALTPLIGIGVITIERAYPLTLGSNIGTTT
                                                                                                                                                         181 TAILAALASPGNALRSSLQIALCHFFFNISGILLWYPIPFTRLPIRWAKGLGNISAKYRW
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopuș.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689
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PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
SEQUENCE 674 AA; 73837 WW; 70CE7520C98E73F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 LEEAQEGODVPVKAPETFDNITISREAGGEVPASDSKTECTAL
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR006209; EGF_like.
InterPro; IPR000005; HTHAraC.
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                                                                                                    61 EPTEVDDPWNLPTLQDSGIXWSERDTKGKILCFFQGIGRLILLLGFLYFFVCSLDILSSA 120
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091237; 013231; 013174;
01.NOV-1996 (TrEMBILE). 01, Created)
01-NOV-1996 (TrEMBILE). 01, Last sequence update)
01-MAR-21093 (TrEMBILE). 23, Last annotation update)
Na/Pi cotransport system protein.
Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
Length 643;
                                                    Indels
57.8%; Score 2080; DB 13;
64.5%; Pred. No. 1.1e-142;
ive 82; Mismatches 117;
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TISSUE=Renal collecting duct, and Intesti
WEDLINE-94346426; PubMed=8067391;
WEDLINE A., Murer H., Kinne R.K.;
"Cloning and expression of a renal Na-Pi
flounder.";
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Best Local Similarity 64.5
Matches 401; Conservative
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                                                    56 ATL---IDEPTEVDDPWNLPTLQDSGIKWSERDTKGKILCFPQGIGRLILLLGFLYFFVC 112
                                                                                    172
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       5
                                                                                                                                                                                                                                                                                                                                                                                      WDFLPKWMHSLKPWDACMLGASLWCKQF-CCCCGKHCKGC-----KCC---KCCHDK
                                                                                                                                                                                KNKSLVKIWCKTFTNKTQINVTVPSTANCTSPSLCWTDGIQNWTMKNVTYKENI----AK
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                                                                                                                                                           SLDILSSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIGVLVTVLVQSSSTSTSTVVSMVSS
                                                                                                                                                                                                                                                                                                                                                              VEVATHYLEIITQLIVESFHFKNGEDAPDLLKVITKPFTKLIVQLDKKVISQIAMNDEKA
                                                                                                                                                                                                                                                          SLITVRAAIPIIMGANIGTSITNTIVALMQVGDRSEFRRAFAGATVHDFFNWLSVLVLLP
       ---- GTPSDPEK-ELSPTYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinus carpio (Common carp).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
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TISSUE-Kidney,

Merner A., Kinne R.K.H. Jr.;

Merner A., Kinne R.K.H. Jr.;

Submitted (AMC-2000) to the EMEL/GenBank/DDBJ databases.

R EMEL, AF297189; AAG35803.1; -.

R InterPro; IRR003841; Na/Pi corranspt.

Pfam; PF02690; Na Pi corrans; 2.

R TICRFAMS; TICRO1013; 2a58; 1.

NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBirel. 16, Created)
01-MAR-2001 (TrEMBirel. 16, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
Na/Pl cotransporter Napi-IID2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : : | | : : | | : EDBECDIETKPQALEWHDNV-IDLSDEIKKPESDEQ 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEAQEGODVPVKAPETFDNITISREAQGEVPASDSK 683
       MPPFPEIDNHGFNTGDYVDDSKPVWSTGINPVPND--
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82 SERDTKGKILCFFQGIGRLILLGFLYFFVCSLDILSSAPQLVGGKMAGQFFSNSSIMSN 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 TPDALCWYDGDLIWTQKNQTDTIYLKKCTHMFVPADLPDLAVGLILLALSLLALCTCLIL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 IVKILINSMIKGQVAVVIKKVINTDFPPPRAWTGYLALIVGAGMTFIVQSSSVFTSAITP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVGDRSEFRRAFAGATVHDFFNWLSVLVLLPVEVATHYLEIITQLIVESFHFKNGEDAPD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 LLKVITKPFTKLIVQLDKKVISQIAMNDEKAKNKSLVKIWCKTFTNKTQINVTVPSTANC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSPSLCWTDGIQNWTWKNVTYKENIAKCQHIFVNFHLPDLAVGTILLILSLLVLCGCLIM 381
                                                                                                                                                                                                                                                                                                                                                                                2 SGSPPGA----DADKHEPQTPIRILSPWPAQQWE---PEQEBEVDPWELPELDIGVKW 53
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                                                                                                                                                                                                                                                                                                                                                              22 AGQQPTAPDKSKETNKNNTEAPVTKIELLPSYSTATLIDEPTEVDDPWNLPTLQDSGIKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 IVLAIFVIVVNVMOKRCPRFLPSFIRSMEFLPKPLHSLKPWDRVVTAGMSFCRTRCCCCC
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
Cyprinidae; Danio.
UNEL_TaxID=7955;
                                                                                                          Kinne R.K.H.
                                                                                                                                                                                                                                                                                              Length 632;
                                                                                    TISSUE-Kidney;
Nalbant P., Schoelermann B., Dehmelt L., Hentschel H., K
Graham C., Werner A.;
Graham C., Werner A.;
Schoelermer A.;
Submitted C., Werner A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF297180, AAG3556.1;
EINTERPO, IPRO03841; Na/Pi_cotranspt.
Pfam; PF02690; Na_Pi_cotranspt.
TIGREMAS; TIGRO1013; 2a58; 1.
                                                                                                                                                                                                                                                             632 AA; 68983 MW; FEEC84E8F0270B91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created) (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                            56.9%; Score 2047; DB 13;
61.2%; Pred. No. 2.8e-140;
tive 86; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 631 AA
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Matches 403; Conservative
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01-MAY-2000 (
01-MAR-2003 (
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SEQUENCE
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Q9PTQ8
ID Q9PTQ1
AC Q9PTQ1
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DT 01-MAN
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                                                                                                                                                                                                                                                                                                                                                                                               ELDTKGKAMRVLTGLLKLVALIGLLYFFICSLDVLSSAFQLVGGKAAGDIFKDNAVLANP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGLVIGVLVTVLVQSSSTSTSTVVSMVSSSLLTVRAAIPIIMGANIGTSITNTIVALMQ 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKILGSVLKGQVATVIKKTINTDFPFPRAMLTGYLAILVGAGMTFIVQSSSVFTSALTPL 442
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                                                                                                                                                                                                                                                                                                                                  2 APRQKVGTNSSPKPALDDDAPVGNIP--PAYSTLDLVSDPDA-DPWNAPRLIDNGVKWS 58
                                                                                                                                                                                                                                                                                                              82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536 VLIVFVIVVNVMQSRCPRFLPRVLQDWDFLPRPLHSMAPWDTVVTSALGFCGKYCCCC-
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                                                                                                                                                                                                                                                                                                              28 APDKSKETNKN-----NTEAPVIKIELLPSYSTATLIDEPTEVDDFWNLPTLQDSGIKWS
                                                                                                                                                                                                                                                                            32; Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TREMBLrel. 23, Last annotation update)
01-MAP-2003 (TREMBLrel. 23, Last annotation update)
Ma/Pi corransporter NaPi-IID2 (Eragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCCRACCLLCGCPKCCRCSKCCEDLEBAOEGODVPVKAPETFDNITISRE
                       Kohl B., Wagner C.A., Hulseweh B., Busch A.E., Werner A.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                     [3]
SEQUENCE FROM N.A.
Strunck U., Rimpel H., Werner A.;
Strunck G.SE-1996) to the EMEL/GenBank/DDBJ databases.
Submitted (SEP-1996) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                    Interpro; IPR003841; Na/Pi_cotranspt.
PERM; PP02690; Na_Pi_cotrans; 2.
TIGRRAMs; TIGR010[3; 2a58; 1.
SEQUENCE 636 Aa, 69240 NW; 60EA81699C6807A1 CRC64;
                                                                                                                                                                                                                                         Query Match 57.2%; Score 2058; DB 13; Best Local Similarity 62.0%; Pred. No. 4.5e-141; Matches 403; Conservative 90; Mismatches 125;
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       SEQUENCE FROM N.A.
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InterPro; IPR003841; Na/Pi_cotranspt.
Pfam; PF02690; Na_Pi_cotrans; 2.
TIGRFAMS; TIGRO1013; 2ac8; 1.
SEQUENCE 637 AA; 68732 WW; D4091C
                                                                                (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Kidney; MEDLINE=21085660; PubMed=11217851;
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    PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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01-JUN-2001 (
01-MAR-2003 (
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                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI TaxID=7955;
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                                                                                     3rachydanio rerio (Zebrafish) (Danio rerio).
    II Na/Pi cotransport system protein.
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                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Intestine;
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Strausberg R.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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Solute carrier family 34 (Sodium phosphate), member 1.
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